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FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
PRIOR APPLICATION NUMBER: JP 106006/95
PRIOR APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106010/95
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PRIOR APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
PRIOR APPLICATION NUMBER: JP 106011/95
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER:
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF DETECTING ANTI-CHLAMYDIA PNEUMONIAE ANTIBODY USING TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE-SPECIFIC ANTIGENS FILE REFERENCE: 1254-0168P CURRENT APPLICATION NUMBER: US/09/689,913A CURRENT FILING DATE: 2000-10-12 NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 259
TYPE: PRT
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TITLE OF INVENTION: METHOD FOR DETECTION AND/OR MEASUREMENT
FILE REFERENCE: 1254-0166P
CURRENT APPLICATION NUMBER: US/09/689,914A
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 259
TYPE: PRT
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                             Sequence 5, Application US/09689916A Patent No. 6491924 GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
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Pred. No. 0.002;
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                                             FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR ADDITE: 28-APR-1995
PRIOR ADDITE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,326A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                           APPLICATION NUMBER: JP 224
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
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ADDRESSEE: Pennie & Eder STREET: 1155 Avenue of CITY: New York
STATE: New York
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APPLICANT:
APPLICANT:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                          PRIOR APPLICATION DATA:
            APPLICATION NUMBER: FILING DATE: 28-AP
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ZIP: 10036-2711
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Similarity 100.0%;
L4; Conservative (
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28-APR-1995 INFORMATION:
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oto, Akira
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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RESULT 7
US-09-689-913A-2; Sequence 2, Application US/09689913A; Sequence 2, Application US/09689913A; Patent No. 6489122; GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD OF DETECTING ANTI-CHLAMYDIA PNEUMONIAE ANTIBODY USING; TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE-SPECIFIC ANTIGENS
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                                                                      FILE REFERENCE:
CURRENT APPLICAT
CURRENT FILING DI
NUMBER OF SEQ ID
SOFTWARE: Patent
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD FOR DET
FILE REFERENCE: 1254-0166P
CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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Best Local
Matches 1
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                                LENGTH: 271
TYPE: PRT
ORGANISM: Ar
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OTHER IN
         OTHER INFORMATION:
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REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 74;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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LENGTH: 271 amino acid
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[CATION NUMBER: US/09/689,913A
                                                                                                  ID NOS:
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Pred. No. 0.0
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US-09-689-916A-2
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Matches 14
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Best Local
Matches 1
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GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC
FILE REFERENCE: 1254-0167P
CURRENT APPLICATION NUMBER: US/09/689,916A
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
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                       ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                  TITLE OF INVENTION: MEATITLE OF INVENTION: PHE NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penning
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ORGANISM: Artificial
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TITLE OF I
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                                                                                                                                                                                                                                                                       TITLE
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CITY: 1
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COUNTRY:
APPLICATION NUMBER: FILING DATE: 19-MA
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Similarity 100.0%;
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larity 100.0%;
Conservative
                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                     Matsumoto,
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ra, Kazuhiko
sumoto, Akira
ion: Chlamydia pneumoniae antigenic polypeptides, dnas coding
sumoto, Akira
ion: Chlamydia pneumoniae antigenic polypeptides, dnas coding
ion: Fused proteins containing the polypeptides, dnas, transformants
ion: Fused proteins containing the recombinant vectors carrying the dnas, transformants
ion: Containing the recombinant vectors, method for production of
containing the recombinant vectors, method for measurement
fion: Antibody, method and reagents for diagnosis of chlamydia
fion: Pneumoniae infections, probes and primers for detection and/or
preagents for detection and/or measurement of chlamydia

pragents for detection and/or measurement of chlamydia
9-MAR-1997
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Pred. No.
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SEQ ID NO 1
LENGTH: 4
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Matches
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Sequence 16, Application US/09689914A
Patent No. 6485914
GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD FOR DETECTION AND/OR MEASUREMENT OF FILE REFERENCE: 1254-0166P
CURRENT APPLICATION NUMBER: US/09/689,914A
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
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INFORMATION
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ORGANISM: Artificial
FEATURE:
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APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
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FILING DATE: 28-AP
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Similarity 100.0%;
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FOR SEQ ID NO:
CHARACTERISTICS:
432 amino acid
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ATION NUMBER: 24,576
CE/DOCKET NUMBER: 7426
NICATION INFORMATION:
NE: (212) 790-9090
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PELPKPGVTPRS
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28-APR-1995
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                                            Score 76; DB 4;
Pred. No. 0.0034;
Mismatches 0;
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US-09-689-913A-16
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GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD OF DETECTING ANTI-CHLAMYDIA PNEUMONIAE
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE-SPECIFIC ANTIGENS
FILE REFERENCE: 1254-0168P
CURRENT APPLICATION NUMBER: US/09/689,913A
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CHLAMYDIA FILE REFERENCE: 1254-0167P CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2000-10-NUMBER OF SEQ ID NOS: 33
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                                 APPLICANT: Izutau,
APPLICANT: Izutau,
APPLICANT: Obara,
APPLICANT: Matsumo
TITLE OF INVENTION:
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ORGANISM: Artificial
FEATURE:
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ORGANISM: Artificial
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LENGTH: 432
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Similarity 100.0%;
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Matsumoto, Akira

/ENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,

/ENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING

/ENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS

/ENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF

VENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT

VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
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larity 100.0%;
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oto, Akira
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Pred. No.
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Pred. No.
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US-09-689-914A-

Sequence

Patent No. 6485914
GENERAL INFORMATION:

pplication US/09689914A 85914

APPLICANT: Hiroshi IZUTSU et al TITLE OF INVENTION: METHOD FOR IFILE REFERENCE: 1254-0166P

DETECTION AND/OR MEASUREMENT OF

CHLAMYDIA

PNEUMONIAE

CURRENT

APPLICATION NUMBER: US/09/689,914A

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Matches
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REFERENCE/DOCKET NUMBER: 7426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
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COMPUTER READAE
MEDIUM TYPE:
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APPLICATION NUMBER:
FILING DATE: 20-SEP-
PRIOR APPLICATION DATA:
                                                                                                                   MOLECULE
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                                                            Local
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                                                                                                                                             TYPE:
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DATE: 28-APR-1995
PLICATION DATA:
                                                                                                                  TYPE:
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1155 Avenue of the Americas
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                                                Score 76; DB 3;
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Sequence 1, Application US/09689916A; Patent No. 6491924; GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIFILE REFERENCE: 1254-0167P; CURRENT APPLICATION NUMBER: US/09/689,916A; CURRENT FILING DATE: 2000-10-12; NUMBER OF SEQ ID NOS: 33; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09689913A; Patent No. 6489122; GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD OF DETECTING ANTI-
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE-SPIFILE REFERENCE: 1254-0168P
CURRENT APPLICATION NUMBER: US/09/689,913A; CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 33
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US-09-689-913A-1
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                                                                                      TYPE: PRT
ORGANISM: Chlamydophila
09-689-916A-1
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TYPE: PRT
ORGANISM: Chlamydophila
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Pred. No.
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APPLICANT: The Regents of the University of California; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence; FILE REFERENCE: 018941-000411US; CURRENT APPLICATION NUMBER: US/09/438,185A; CURRENT FILING DATE: 2002-03-13; PRIOR APPLICATION NUMBER: US 60/108,279; PRIOR FILING DATE: 1998-11-12; PRIOR FILING DATE: 1998-11-12; PRIOR FILING DATE: 1999-04-08; NUMBER OF SEQ ID NOS: 1074; SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-198-452A-8
RESULT 19
US-08-809-326A-
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Sequence 867, Application:
Patent No. 6559294

GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmitte OF INVENTION: thereof and uses thereof, in particular for the diagnosis, TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
CURRENT FILING DATE: 1998-11-24
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SEQ ID NO 867
LENGTH: 496
TYPE: PRT
ORGANISM: Chl
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Best Local
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TYPE: PRT
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Sequence 15, ...; Sequence 15, ...; Patent No. 6165478; Patent No. 6165478 Trutsu,

Application .65478

US/08809326A

APPLICANT:

Izutsu, Hiroshi Obara, Kazuhiko Matsumoto, Akira

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               RESULT 20
US-09-689-914A-15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 649 amin
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mills Charlor
                                                                                                                                                                                                                                                                                                                   NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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ZIP: 10036-2711
COMPUTER READABLE FOR MEDIUM TYPE: Flo
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APPLICATION NUMBER: JP :
FILING DATE: 20-SEP-199
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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New York
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
PNEUMONIAE GENE
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RESULT 22
US-09-689-916A-
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US-09-689-913A-
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FILE REFERENCE: 1
CURRENT APPLICATION OF SEQ ID NUMBER OF SEQ ID NO 15
SEQ ID NO 15
                                                                                                                                              Sequence 19 Patent No.
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Best Local S
Matches 14
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Best Local S
Matches 14
                       SEQ ID NO :
                                                                           GENERAL INFORMATION:

APPLICANT: Hiroshi IZUTSU et al.

TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE

FILE REFERENCE: 1254-0167P

CURRENT APPLICATION NUMBER: US/09/689,916
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ORGANISM: Artificial 9
FEATURE:
OTHER INFORMATION: fue
5-09-689-914A-15
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GENERAL INFORMATION:
APPLICANT: Hiroshi IZUTSU et al.
TITLE OF INVENTION: METHOD FOR DETECTION AND/OR MEASUREMENT
FILE REFERENCE: 1254-0166P
CURRENT APPLICATION NUMBER: US/09/689,914A
CURRENT FILING DATE: 2000-10-12
                                                          CURRENT APPLI
CURRENT FILIN
NUMBER OF SEQ
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                                              SOFTWARE:
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SOFTWARE: PatentIn version
SEQ ID NO 15
ORGANISM:
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ORGANISM: Artificial
             TYPE:
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                                                                                                                                                 64
                                               Patent In
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RESULT 24
US-09-270-767-47482
; Sequence 47482, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47482
; LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-270-767-32265

US-09-270-767-32265; Application US/09270767; Sequence 32265, Application US/09270767; Patent No. 6703491; GENERAL INFORMATION:

APPLICANT: Homburger et al.; TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094; CURRENT APPLICATION NUMBER: US/09/270,767; CURRENT FILING DATE: 1999-03-17; NUMBER OF SEQ ID NOS: 62517; SOFTWARE: Patentin Ver. 2.0
RESULT 25
US-09-902-54
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LENGTH: 243
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APPLICANT: Slater, Gregory J.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genor

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10741

LENGTH: 175
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US-09-252-991A-
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US-08-750-152A-
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LENGTH: 671
TYPE: PRT
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GENERAL INFORMATION:
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CATION NUMBER: US 60
G DATE: 1998-07-27
EQ ID NOS: 33142
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           SEQUENCES: 1
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                                                          ASAKURA, YOKO
KIMURA, EIICHIRO
ABE, CHIZU
KAWAHARA, YOSHIO
                                  KAWAHARA, YOSHIO
NAKAMATSU, TSUYOSHI
ENTION: ALPHA-KETOGLUTARATE
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ON: NUCLEIC ACID AND AMINO ACID

ON: AERUGINOSA FOR DIAGNOSTICS A

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Pred. No. 1.8e+02;
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US-09-252-991A-26874
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RESULT 29
US-09-252-991A-27499
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US-09-252-991A-26874
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SE

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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LENGTH: 236
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Marc J.
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
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CITY: AF
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Pred. No. 3.5e
3; Mismatches
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Pred.
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Patent No. 63222.

Patent No. 63222.

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et 12.

APPLICANT: Marc J. Rubenfield et 12.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AND TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTION FILLE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                  RESULT 31
US-09-252-991A-2
; Sequence 29789
; Patent No. 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR APPLICATION NUMBER: US 60/094,190; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 27499; LENGTH: 261; TYPE: PRT
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US-09-252-991A-
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GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                   GENERAL
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       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991.2
CURRENT FILING DATE: 1999-02.10
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                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: P
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9-252-991A-27499
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OF INVENTION:
OF INVENTION:
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17180
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51795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Rubenfield et al.
NN: NUCLEIC ACID AND AMINO ACID SEQUENCES
NN: AERUGINOSA FOR DIAGNOSTICS AND THERAPE
107196.136
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N: NUCLEIC ACID AND AMINO ACID

N: AERUGINOSA FOR DIAGNOSTICS F

107196.136
1998-02-18
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Pred. No.
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Pred. No. 2.
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2.7e+02;
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SOFTWARE: FastSE(
SEQ ID NO 23
LENGTH: 247
TYPE: PRT
ORGANISM: Homo s
US-08-951-822-23
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US-08-951-822-23
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                                                                                                                                                                                                                                                  RESULT 33
US-08-705-245-
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APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20
CURRENT APPLICATION NUMBER: US/08/951,822A
CURRENT FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 36
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LENGTH: 159
TYPE: PRT
ORGANISM: Pseuc
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GENERAL INFOR
APPLICANT:
TITLE OF IN
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Best Local S
Matches 8
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-09-252-991A-29789
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GENERAL INFORMATION:
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Best Local
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                                                                                                 NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P
STREET: 4225 Executive Square,
CITY: La Jolla
STATE: CA
                                                                                                                                                                         APPLICANT: Nathans
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                          COUNTRY:
ZIP: 920
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R OF SEQ ID NOS: 33142
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Conklin,
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Darrell
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FIBROBLAST GROWTH FACTOR HOMOLOGOUS
FACTORS (FHF8) AND METHODS OF USE
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72.7%;
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e, Suite
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               Version
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1.2e+02;
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; SOFTWARE: Fasi
; SEQ ID NO 23
; LENGTH: 247
; TYPE: PRT
; ORGANISM: HOU
US-09-368-951-23
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US-08-705-245-4
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US-09-390-207-1
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US-09-368-951-2
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Best Loc
Matches
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Patent No
GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: US/08/705,245
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/094001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-50999
NFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS: no*
TOPOLOGY: ''
OLECIT'
                                                                                                                                                                                                   Query Ma
Best Loc
Matches
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
                                                                        Sequence 16, Patent No. 6
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INFORMATION F
SEQUENCE CH
LENGTH:
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CURRENT APPLICATION NUMBER: US/09/368,951
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 08/951,822
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 36
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
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Conservative
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Darrell
Fenella
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                                                                                                                                                                                                   Score 42; DB Pred. No. 1.2e 1; Mismatches
                                                                                                                                                                                                                                                                                                                  Version 3.0
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US-09-229-947-23
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                                                                                                                    Patent No. 6635744

GENERAL INFORMATION:
APPLICANT: Nathans et al TITLE OF INVENTION: FIBSTITLE OF INVENTION: FACTOR SEPONDENCE ADDRESS:
ADDRESSEE: Fish & Rich STREET: 4225 Executive CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HC
FILE REFERENCE: 96-20C1
CURRENT APPLICATION NUMBER: US/C
CURRENT FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Ve
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Best Local S
Matches
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NUMBER OF SE
SOFTWARE: Pa
SEQ ID NO 16
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Matches
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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9-229-947-23
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                           STATE:
                                                                                                 COUNTRY:
                                                                                                                                                                                                     ce 4, Application US/09490714
No. 6635744
AL INFORMATION:
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Raymond, Fenella
Bukowski, Thomas R.
Holderman, Susan D.
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                                                                                                                               E: Fish & Richardson P
4225 Executive Square,
                                                                                                                                                             Nathans et al., Jeremy
PENTION: FIBROBLAST GROWTH FACTOR
PENTION: FACTORS (FHFs) AND METHOR
PROJUBULES: 37
                                                                                                 USA
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"OVEL FGF HOMOLOGS
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/949, CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 9554
LENGTH: 247
TYPE: PRT
                                     RESULT 39
US-08-462-169B-
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US-09-949-016-91
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Matches 7
Patent No. 5773252
GENERAL INFORMATION:
                       Sequence
                                                                                                                                         Matches
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Patent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-50999
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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9-490-714-4
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: 25-JAN-2 CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                        Local
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STRANDEDNESS:
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1; Mismatches
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Pred. No.
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APPLICANT: TITLE OF IN

CANT: John Gree
OF INVENTION:
R OF SEQUENCES:

Greene and Craig A. Rosen DN: Fibroblast Growth Factor-15 CES: 32

NUMBER

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COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,169

FILING DATE: 05 JUN 95

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-4

TELECOMMUNICATION INFORMATION:

TELEFAX: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-462-169B-2
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US-08-462-169B-23
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Best Loc
Matches
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ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,1698
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-441 (FTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: John Greene and Craig A. Rosen TITLE OF INVENTION: Fibroblast Growth Factor-15 NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA
ADDRESSEE: CECCHI,
STREET: 6 BECKER F.
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CAI
ADDRESSEE: CEI
STREET: 6 BECI
CITY: ROSELANI
STATE: NEW JEI
COUNTRY: USA
ZIP: 07068
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5. 5773252
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ESSEE: CECCHI, STEWART &
ET: 6 BECKER FARM ROAD
: ROSELAND
E: NEW JERSEY
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7; Conservative
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CECCHI, STEWART
BECKER FARM ROAD
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                                        (PF203)
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; STRANDEDNESS:
; TOPOLOGY: LINE
; MOLECULE TYPE: F
US-08-462-1698-23
                                           Query Match
Best Local S
Matches 7
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                                                                                                                                    TYPE:
                                          Similarity 7; Conserv
                                                                                                                                 AX: 201-994-1744
ON FOR SEQ ID NO: 2:
E CHARACTERISTICS:
H: 252 AMINO ACIDS
AMINO ACID
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                PKPGVTP 12
KPGVTP 230
                                         55.3%;
ilarity 87.5%;
Conservative
                                                                                                    LINEAR
: PROTEIN
                                                                                                                                                                       23:
                                          Score 42; DB 1; Length 25; Pred. No. 1.3e+02; Mismatches 0; Indels
                                                                 Length 252;
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Search completed: October 28, 2005, 22:19:31 Job time : 39.7391 secs

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Title:
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Sequence:
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Maximum
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RP SEQUENCE FROM N.A.

STRAIN=TW-183; RA Schnbmacher A., Muehldorfer I., Bensch K.W., Schaefer P. Schneider S., Pohl T., Essig A., Marre R., Melchers K.; "The genome sequence of Chlamydia pneumoniae TW183 and comparison other Chlamydia strains based on whole genome sequence analysis."; L Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases."; MEDLINE=207777".

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Q9JS66; Q7AI93; Q7BWY2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4 Hypothetical protein CP1062 (Hypothetical protein CP)
5 OrderedLocusNames=CP1062, CPJ0809, CpB0838;
6 Chlamydia pneumoniae (Chlamydophila pneumoniae).
8 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaceae; Chlamydiaceae; Chlamydiales; Chlamydiaceae; Chlamydiac
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Shirai M., Hirakawa H., Kimoto M., Tabuch
Shiba T., Ishii K., Hattori M., Kuhara S.
"Comparison of whole genome sequences of
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AE002263; AAF38835.1; -.
EMBL; AE017160; AAP98767.1; -.
EMBL; AP002548; BAA99017.1; -.
PIR; A81507; A81507.
PIR; G86591; G86591.
TIGR; CP1062; -.
InterPro; IPR000508; Peptidase S26.
PROSITE; PS00501; SPASE_I_1; UNKNOWN_1.
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SEQUENCE 488 AA; 49819 MW; 06F2F0B905
Q9Z797;
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01-MAY-1999 (TrEMBLrel. 10, Created)
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DT 01-JUN-2003 (TrEMBLrel. 15,
DT 01-JUN-2003 (TrEMBLrel. 24,
DE Hypotherical protein TC0867;
GN OrderedLocusNames=TC0867;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; ChlamOX NCBI_TaxID=83560;
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STRAIN=CWL029;

MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;

Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. tra Nat. Genet. 21:385-389(1999).

EMBL; AE001662; AAD18947.1; -.

PIR; F72031; F72031.

InterPro; IPR000508; Peptidase S26.

PROSITE; PS00501; SPASE I 1; UNKNOWN 1.

Complete proteome; Hypothetical protein.

SEQUENCE 493 AA; 50489 MW; 90F315B7A20AC2F0 CRC64;
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Bacteria; Chlamy
NCBI_TaxID=813;
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SEQUENCE FR
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MEDLINE=990
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Mitchell
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"Genome sequence of an obligate intracellular pathogen of Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AE001328; AAC68180.1; -.
PIR; D71497; D71497.
Complete proteome; Hypothetical protein.
SEQUENCE 487 AA; 50217 MW; D4D6038EC1D4A03D CRC64;
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UW-3 / Cx;

000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;

.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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|PELPKPGVTPRS 177
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Pred. No.
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Pred. No. 0.0047;
Mismatches 0;
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C Q9MX74;
ITEMBLrel. 15, Created)
JT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
JT 01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
JE MHC class II alpha chain (Fragment).
Name=Orni-DCA;
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
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P SEQUENCE FROM N.A.

C STRAIN=Mopn / Nigg;

X MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;

A Read T.D., Brunham R.C., Sill S.R., Heidelberg J.F., Whouri H.M., Craven B., Bowman A., Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman A., Bass S., Linher K.D., Nelson W.C., DeBoy R.T., Kolonay J.F., A., McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;

"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).

R PIR; F81655; F81655.

R TIGR; TC0867; -.

Complete proteome; Hypothetical protein.

Complete proteome; Hypothetical protein.
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SEQUENCE FROM N.A.
Murray B.W., Shintani S., Sue
Submitted (DEC-1999) to the E
EMBL; AF214724; AAF66864.1; -
NON TER 1
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SEQUENCE S9 AA; 6184 MW;
Q9MX77;
Q9MX77;
Q9MX77;
Q9MX77;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II alpha chain (Fragment).
Name=Orni-DCA;
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroic Cichlidae; Oreochromis.
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Pred. No. 5.8;
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CE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

CActinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

CC Cichlidae; Oreochromis.

CX NCBI TaxID=8128;

RN (1)

RP SEQUENCE FROM N.A.

Murray B.W., Shintani S., Sueltmann H., Klein J.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases

NR EMBL; AF214726; AAF66866.1; -.

TON TER 1

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C SEQUENCE 62 AA.
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OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RA Murray B.W., Shintani S., Sueltmann H., Klein J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases

NR EMBL; AF214718; AAF66858.1; -.

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2 SEQUENCE 59 AA. 7.
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01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-DEC-2001 (TrEMBLrel. 19, L
MHC class II alpha chain (Fra
Name=Orni-DCA;
Oreochromis niloticus (Nile t
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Q9MX72;
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01-OCT-2000
01-DEC-2001
MHC class II
Name=Orni-DC
Oreochromis
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[1]
SEQUENCE FROM N.A.
Murray B.W., Shintani S., Sueltmann H., Klein
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AF214721; AAF66861.1; -.
NON_TER 1 1
SEQUENCE 59 AA; 6156 MW; CB59D7F288CFB340
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Pred. No. 5.8;
0; Mismatches
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Pred. No.
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C Q9MX79;
C Q9MX79;
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-DCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E MHC class II alpha chain (Fragment).
Name=Orni-DCA;
Name=Orni-DCA;
S Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
C Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
C Cichlidae; Oreochromis.
X NCBI TaxID=8128;
P SEQUENCE FROM N.A.
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Q9MX71;
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alpha chain (Fragment).
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e EMBL/GenBank/DDBJ
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Pred. No. 8.3;
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0; Mismatches
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a; Vertebrata; Euteleostomi;
a; Euteleostei; Neoteleostei;
morpha; Perciformes; Labroidei
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RESULT 13
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AC Q9MX82;
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DE MHC class II
GN Name=Orni-DC
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Murray B.W., Shintani S., Sue

Murray B.W., Shintani S., Sh
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Q9MX76;
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MHC class II
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
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alpha chain (Fragment).
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SEQUENCE FROM N.A.

STRAIN-GPIC;

MEDLINE-22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;

Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.

Heidelberg J.F., Holtzapple E.K., Khouri H.M., Federova N.B.,

Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,

White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,

Bavoil P.M., Fraser C.M.;

"Genome sequence of Chlamydophila caviae (Chlamydia psittaci GP

examining the role of niche-specific genes in the evolution of

Chlamydiaceae.";

Nucleic Acids Res. 31:2134-2147(2003).

R EMBL; AE016997; AAP05693.1; -.

RTIGR; CCA00954; -.

Complete proteome.

SEQUENCE 494 AA; 50829 MW; C544379F027871CB CRC64;
Q82DG2;
Q82DG2;
Q1-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
OrderedLocusNames=SAV5020;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Ac
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Murray B.W., Shintani S., Sue
Submitted (DEC-1999) to the E
EMBL; AF214716; AAF66856.1; -
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SEQUENCE 65 AA; 6835 MW;
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Q82116;
Q82116;
01-JUN-2003 (TrEMBLrel. 201-JUN-2003 (TrEMBLrel
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
NCBI_TaxID=8128;
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Chlamydophila caviae.
Bacteria; Chlamydiae; Chlam
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line NGP.";
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Q9Y2W4;
01-NOV-1999
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Sakaki Y.,
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MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005041; BAC72732.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0000271; P:polysaccharide biosynthesis;
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007267; GtrA.
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genomyces avermitilis.";
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                                                                                                                                                                                                                                                                                                                          PubMed=10729226; DOI=10.1006/geno.1999.6097; A., Corvi R., Dihlmann S., Praml C., Cavenee
                                                                                                                                                                                                                                                                     translocation breakpoint
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20219 MW; 9F8887E94E3AC99B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                    107088 MW;
                                                                                                                                                                                                                                                                                       characterization of novel genes located at the
                                                                            61.8%;
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Pred. No.
                                                          Score 47; DB 2; Li
Pred. No. 2.1e+02;
L; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vo Catarrhini;
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Eukaryota; Metazoa; Chordata; Craniat,
Mammalia; Eutheria; Primates; Catarrh
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Xia J.-h., Ruan Q.-g., Liu C.-y.;
Submitted (JAN-1998) to the EMBL/GenB.
EMBL; AF041104; AAC28264.1; JOINED.
EMBL; AF041096; AAC28264.1; JOINED.
EMBL; AF041099; AAC28264.1; JOINED.
EMBL; AF041099; AAC28264.1; JOINED.
EMBL; AF041100; AAC28264.1; JOINED.
EMBL; AF041101; AAC28264.1; JOINED.
EMBL; AF041101; AAC28264.1; JOINED.
EMBL; AF041102; AAC28264.1; JOINED.
EMBL; AF041103; AAC28264.1; JOINED.
InterPro; IPR002951; Atrophin.
Pfam; PF03154; Atrophin.
PRINTS; PR01222; ATROPHIN.
SEQUENCE 1012 AA; 109047 MW; 5486
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Mammalia; Eutheria; Primates; Ca
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Xia J.-H., Liu C.-Y., Ruan Q.-G.
Submitted (JUL-1997) to the EMBI
EMBL; AF016005; AAC31120.1; -.
InterPro; IPR002951; Atrophin.
Pfam; PF03154; Atrophin-1; 1.
PRINTS; PR01222; ATROPHIN.
SEQUENCE 1012 AA; 108967 MW;
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O43393
PRELIMINARY;
O43393;
O1-JUN-1998 (TrEMBLrel. 06, C)
O1-JAN-1999 (TrEMBLrel. 09, I)
O1-MAR-2004 (TrEMBLrel. 26, I)
Atrophin-1 related protein.
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O75359;
O1-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
01-MAR-2004 (TrEMBLrel. (
Atrophin-1 like protein. Name=ARG;
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Pred. No. 2.2e+02;
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01-MAR-2004 (TrEMBLrel. 26, L
01-MAR-2004 (TrEMBLrel. 26, L
KIAA0458 protein (Fragment).
Name=KIAA0458;
       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Pancreas;
MEDLINE=22388257; Pub
Strausberg R.L., Feir
Klausner R.D., Collir
Altschul S.F., Zeeber
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InterPro; II
InterPro; II
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InterPro; II
Pfam; PF00319
Pfam; PF0032
Pfam; PF0032
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PRINTS; PR01
SMART; SM001
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SEQUENCE FROM TISSUE=Brain MEDLINE=981: Seki N., Oh:
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Q6P6B9;
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RERE protei
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-1- SUBCELLU
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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4:345-349(1997).
ELLULAR LOCATION: Nuclear (By similarity).
007927; BAA32303.2; -.
005634; C:nucleus; TAS.
008267; F:poly-glutamine tract binding; TP.
006607; P:NLS-bearing substrate-nucleus im; IPR002951; Atrophin.
; IPR001005; Myb_DNA_binding.
; IPR001005; Myb_DNA_binding.
; IPR000679; Znf_GATA.
03154; Atrophin-1; 1.
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10717; SANT; 1.
10401; ZnF_GATA; 1.
creas;
388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
R.L., Feingold E.A., Grouse L.H., Derge J.G.,
.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D..F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                            QLPTPGPTP 528
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zation of cDNA clones in size-fractionated
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GATA; 1
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Last annotation update)
                                                                                                                                                                                                                                                                                    Score 47; DB 2; Le Pred. No. 2.8e+02; 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa K., Miyajima N., Nakajima D.,
                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     PRT;
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-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

REMBL; BC062342; AAH62342.1; -.

GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005635; P:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent interpro; IPR001025; BAH.
Interpro; IPR001025; BAH.
Interpro; IPR001005; Myb_DNA_binding.
Interpro; IPR000679; Znf_GATA.

Refam; PF03154; Atrophin-I; 1.

Refam; PF03154; Atrophin-I; 1.

Refam; PF01426; BAH; 1.

Refam; PF00320; GATA; 1.

Refam; PF00320; GATA; 1.

Refam; PF00249; Myb_DNA-binding; 1.

Refam; PF00249; Myb_DNA-binding; 1.

Refam; PF00249; Myb_DNA-binding; 1.

Refam; PF00320; GATA; 1.

Refam
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Q9P2R6;
01-OCT-2000
01-OCT-2000
01-OCT-2003
RERE.
                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=20275632; PubMed=10814707;
MEDLINE=20275632; PubMed=10814707;
MEDLINE=20275632; PubMed=10814707;
Yanagisawa H., Bundo M., Miyashita T., Okan Tokunaga K., Yamada M.; "Protein binding of a DRPLA family through dipeptide repeats is enhanced by extended phum. Mol. Genet. 9:1433-1442(2000).
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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imilarity 72.7%;
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Primates;
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Pred. No. 3.3e+02;
L; Mismatches 2;
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Catarrhini;
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transcription, DNA-dependent;
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T., Okamura-Oho Y
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 similarity)
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; Hominidae;
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Tadokoro
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F.S.W.,
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EMBL; AAAB01008986; EAA00573.

InterPro; IPR001680; WD40.

InterPro; IPR011046; WD40_like
Pfam; PF00400; WD40; 3.

PROSITE; PS00678; WD_REPEATS_
Repeat; WD_repeat.

NON_TER 322 322

SEQUENCE 322 AA; 35311 MW;
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InterPro; IPR001:
InterPro; IPR000:
InterPro; IPR000:
InterPro; IPR000:
InterPro; IPR000:
Pfam; PF01426; B;
Pfam; PF01448; EI
Pfam; PF00320; G;
Pfam; PF00320; G;
Pfam; PF00349; M;
SMART; SM00439; ISMART; SM00401; SMART; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7Q062;
Q7Q062;
Q7Q062;
01-MAR-2004
01-MAR-2004
01-MAR-2004
AgCP9323 (F
Name=agCG55
Anopheles g
Eukaryota;
Neoptera; E
NCBI_TaxID=
[1]
SEQUENCE FR
STRAIN=PEST
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-!- SIMILARIT
-!- CAUTION:
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GO; GO:0005
GO; GO:0005
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105634; C:nucleus; NAS.

105515; F:protein binding; NAS.

1PR002951; Atrophin.

1PR001025; BAH.
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imilarity 72.7%;
Conservative
                                                                                                                                                                                      60.5%;
imilarity 69.2%;
Conservative
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(MAR-2002) to the EMBL/GenBank/DDBJ databases.
RITY: Contains 3 WD repeats.
N: The sequence shown here is derived from an
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Metazoa; Arthropoda; Hexapoda;
                                                                                                                 TPEDTKPGTPPR
                                                                                                                                                                                                                                                                                                                                      IPR001680; WD40.
IPR011046; WD40_like.
400; WD40; 3.
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GATA;
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                                                                                                                                                                                                                                                                                                                  WD_REPEATS_1;
                                                                                                                                                                                                                                                            322
35311 MW;
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                                                                                                                                                                                                                                                                                                                                                                                               EAA00573.1;
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Znf_GATA.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                  UNKNOWN_1.
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era; Culicoidea; Anopheles
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PRELIMINARY;

PRT;

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D QUDU9;
C Q9VDU9;
C Q9VDU9;
T 01-MAY-2000 (TrEMBLrel. 13, Created)
JT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
JT 01-MAY-2000 (TrEMBLrel. 28, Last annotation update)
JT 05-OCT-2004 (TrEMBLrel. 28, Last annotation update)
C C57411-PA (Histamine-gated chloride channel subunit 2) (Histamine-gated chloride channel subunit)
E gated chloride channel subunit 1) (Histamine-gated chloride channel subunit A).

Name=ort; Synonyms=Histl, hclA; ORFNames=CG7411;
C Name=ort; Synonyms=Histl, hclA; ORFNames=CG7411;
C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
C Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
C Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
C NcBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.I

An H.J., Andrews-Pfannkoch C., Baldwin
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EMBL; AY422812; AAR33080.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0045211; C:postsynaptic membrane; IEA.

GO; GO:0005230; F:extracellular ligand-gated io

GO; GO:0004890; F:GABA-A receptor activity; IEA.

GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005216; F:neurotransmitter receptor act

GO; GO:0005216; P:ion transport; IEA.

GO; GO:0007268; P:synaptic transmission; IEA.

InterPro; IPR006028; GABAA recept.

InterPro; IPR006201; Neur_channel.

InterPro; IPR006202; Neur_channel.

PRINTS; PR00253; GABAARECEPTR.

PRINTS; PR00253; GABAARECEPTR.

PRINTS; PR00252; NRIONCHANNEL.

TIGRFAMS; TIGR00860; LIC; 1.

PROSITE; PS00236; NEUROTR ION_CHANNEL; UNKNOWN_ION transport; Ionic channel; Postsynaptic memb

Transport.

485 AA; 55550 MW; 62DFD3849E3747C5
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I Science 287:2185-2195(Zuvv.)

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REQUENCE FROM N.A.

REDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern...

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

"Finishing a whole-genome shotgun: Release 3 of the Drosophila

melanogaster euchromatic genome sequence.";

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Carlson J., Svirskas R.

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  Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
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L. Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

No SEQUENCE FROM N.A.

MEDLINE=22426070; PubMed=12537573;

NA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,

Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

A shburner M., Celniker S.E.;

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"a genomics perspective.";

L. Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

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MEDLINE=22426069; PubMed=12537572;

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A Misra S., Crosby M.A., Mungall C.J., Bayraktaroglu L., Berman B.P.,

A Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,

A Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

J. Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

The Matthews B.B., Carlson B.P.,

M. Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Williams S.
Yeh R.F., Z
Zheng X.H.,
Gibbs R.A.,
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SEQUENCE
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K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Lobup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
K.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
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N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
D., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
OV G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ms. S.M., Woodage W., Zhou X., Zhou S., Zhou X., Smith H.O.,
R.A., Myers E.W., Rubin G.M., Venter J.C.;
enome sequence of Drosophila melanogaster.";
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EMBL; AF382403; AAL66188.1; -.

EMBL; AF411340; AAL05873.1; -.

EMBL; AF435469; AAL74413.1; -.

EMBL; AF435469; AAL74413.1; -.

EMBL; AY049774; AAL12210.1; -.

HSSP; P23415; IMOT.

FlyBase; FBgn0003011; ort.

GO; GO:0030534; P:adult behavior; IMP.

GO; GO:0045472; P:response to ether; IME.

GO; GO:0045472; P:response to toxin; IME.

InterPro; IPR006028; GABAA_recept.

InterPro; IPR006201; Neur_channel.

InterPro; IPR006202; Neur_channel.

Pfam; PF02931; Neur_chan_LBD.

Pfam; PF02931; Neur_chan_LBD; 1.

Pfam; PF02931; Neur_chan_LBD; 1.

Pfam; PF02931; Neur_chan_LBD; 1.

PRINTS; PR00253; GABAARECEPTR.

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"Two cDNAs coding for hista
melanogaster.";
Nat. Neurosci. 5:11-12(2002
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STRAIN#Oregon R;
Yin Z., Skingsley D.R., Ger
Semenov E.P., Hardie R.C.,
Submitted (AUG-2001) to the
-1- SUBCELLULAR LOCATION: 1
Q6CAYO;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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ORFNames=YALIOC23452g;
Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascomycota
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Zheng Y., Hi
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rg B., Yuan J.,
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Vang A.P., Hunt D.C., Ludmerer
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SEQUENCE FROM N.A.
STRAIN=CLIB99;
Genoscope;
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Submitted (JUL-2004) to the EMB EMBL; CR382129; CAG82502.1; -.
InterPro; IPR004829; Csurface a ProDom; PD153432; Csurface anti-SEQUENCE 830 AA; 85939 MW;
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Despons L.,
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Dujon B., Sho
Lafontaine I
Goffard N., 1
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Boisrame A.
                                                                                                                                                                                                                                                                                                             Roy
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                   koff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., ley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., C., Glass L., Orbach M.J., Berglund J., Voelker R., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; Requence of the Filamentous Fungus Neurospora crassa.";
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cetidae; Sordariales;
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M., Anthouard V., Babour A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebr
Actinopterygii; Neopterygii; Teleostei; Euteleo
Acanthomorpha; Acanthopterygii; Percomorpha; Pe
Cichlidae; Oreochromis.
NCBI_TaxID=8128;
[1]
SEQUENCE FROM N.A.
Murray B.W., Shintani S., Sueltmann H., Klein J
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ d
EMBL; AF214728; AAF66868.1; -.
NON_TER 1 1
SEQUENCE 59 AA; 6168 MW; CB59D964C32FB340 C
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Eukaryota; Metazoa; Nematoda; Chror Rhabditidae; Peloderinae; Caenorhab NCBI_TaxID=6239;
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Q9MX70;
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01-OCT-2000 (TrEMBL)
01-OCT-2000 (TrEMBL)
01-DEC-2001 (TrEMBL)
MHC class II alpha (Name=Orni-DCA;
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EMBL; AABX01000008; EJ
InterPro; IPR009058; USEQUENCE 886 AA; 10
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Science 282:2012-2018(1998)
[2]
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3; Wing hlx DNA

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Best Local
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Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wedler H., Lauber Kiewitz C., Eisen Fraser C.M.; "Complete genome & metabolically versenviron. Microbiol EMBL; AE016778; AJ TIGR; PP1101; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q88NV3;
Q88NV3;
01-JUN-2003 ('01-JUN-2003 ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('01-JUN-200) ('
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                                                           Q7XAM1;
Q7XAM1;
Q1-OCT-2003
01-OCT-2003
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Proline-ric
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SEQUENCE FR
MEDLINE=224
Nelson K.E.
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Complete
SEQUENCE
    Name=OJ163
Oryza sati
Eukaryota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonadaceae;
NCBI_TaxID=160488;
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8; Conservative
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Y113G7A.11; CE23282.
08146; F:sulfotransferase activity;
IPR000863; Sulfotransferase.
0685; Sulfotransfer_1; 1.
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Proteobacteria; Gammaproteobacteria;
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va (japonica cui
Viridiplantae;
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h protein family-like protein.
B10.111;
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   (japonica cultivar-group).
ridiplantae; Streptophyta;
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9128 MW; 0E44364E05086EF4 CRC64;
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Pred. No. 1.7e+02;
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      Embryophyta;
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     Tracheophyta;
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Best Local
Matches
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NCBI_TaxID=39947;
[1]
SEQUENCE FROM N.A.
Sagaki T., Matsumoto T., Yamamoto K
"Oryza sativa nipponbare(GA3) genom.
clone:OJ1634_B10.";
Submitted (JUL-2001) to the EMBL/Ge;
EMBL; AP003840; BAC81167.1; -.
Gramene; Q7XAM1; -.
SEQUENCE 152 AA; 16298 MW; 70B5
Buell R.;
Submitted (OCT-2003) to the EMBL/
EMBL; AC133007; AAO60030.1; -.
EMBL; AC139172; AAR01751.1; -.
HSSP; O80337; 2GCC.
Gramene; Q84TW0; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription f
GO; GO:0006355; P:regulation of t
InterPro; IPR001471; TF ERF.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
                                                                                                                                                                                                                                                   SEQUENCE F
Buell R.;
Submitted
[3]
SEQUENCE F
                                                                                                                                                                                                                                                                                                               Yang Q.Q., White O., Submitted [2]
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SEQUENCE
Buell C.R
Overton I
                                                                                                                                                                                                                                                                                                                                                                                                                        Q84TW0;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative AP2 domain containing protein (Putative AP2 domain transcription factor).
Name=OSJNBa0094J08.32; Synonyms=OSJNBb0042K11.4;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                            [4]
SEQUENCE
                                                                                                                                                                    White O., Submitted
                                                                                                                                                                                       SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansbel
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansbel
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansbel
Overton II L.L., Tsitrin T., Kim M.M., Bera J.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V.,
Vanaken S.S., Riedmuller S.B., Utterback T.T.,
Vanaken S.S., Riedmuller S.B., Peterson J.J.,
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Overton II L.L., Tsitrin T., Kim M.M., Bera J.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V.,
Vanaken S.S., Riedmuller S.B., Utterback T.T.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J.,
White O., Salzberg S.L., Fraser C.M.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ (
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White
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leae; Oryzeae; Oryza.
)=39947;
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Conservative
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Fraser C.M.;
he EMBL/GenBank/DDBJ
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Pred. No. 87;
1; Mismatches
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genomic
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T., Feldblyum
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Hsiao J., Blu
Feldblyum T.V
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T.V.,
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EMBL; AKO55045; BAB70844.1; -.

ROG; GO:0005875; C:microtubule associated complex; IEA.

GO; GO:0005875; C:microtubule associated complex; IEA.

GO; GO:0005875; C:microtubule associated complex; IEA.

ROG; GO:0005774; F:motor activity; IEA.

RInterPro; IPR002453; Beta_tubulin.

InterPro; IPR001752; kinesin_motor.

R InterPro; IPR010989; t-snare.

Pfam; PF00225; Kinesin; 1.

R MART; SM00129; KISC; 1.

R PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE; PS00228; TUBULIN_B AUTÖREG; UNKNOWN_1.

ATP-binding; Microtubule; Motor protein.

SEQUENCE 299 AA; 32600 MW; 48934978E5D7E08C CRC64;
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Togiya S.,
Musashino K
Yoshikawa Y
Moriya S.,
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Nakagawa S.
Hishigaki H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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l protein FLJ30483.
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yashi K., Sato H., N
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Submitted (JUL-2004) to the EMBL/GenBank/
EMBL; CR382137; CAG88417.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004413; F:homoserine kinase activ
GO; GO:0016310; F:kinase activity; IEA.
GO; GO:0016310; P:phosphorylation; IEA.
GO; GO:0016310; P:phosphorylation; IEA.
GO; GO:0016310; P:phosphorylation; IEA.
InterPro; IPR006203; GHMP_kinase_ATP.
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR000870; Homoser_kin.
Pfam; PF00288; GHMP_kinases; 1.
PIRSF; PIRSF000676; Homoser_kin; 1.
PRINTS; PR00958; HOMSERKINASE.
TIGRFAMs; TIGR00191; thrB; 1.
PROSITE; PS00627; GHMP_KINASES_ATP; UNKN
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Pred. No. 1.7e+02;
Mismatches
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A Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

R Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

T "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).

N [5]

P SEQUENCE FROM N.A.

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STRAIN=C57BL/6J; TISSUE=Bone;

K MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

K MEDLINE=2053091; PubMed=11076861; DOI=10.1101/gr.152600;

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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090
             Kurihara (
Nishi K.,
Saito R.,
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[4]
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Bone;
Adachi J., Aizawa K., Akimura
Fukuda S., Furuno M., Hanagak
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                                                                                                                              a K., nay
Imotani
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2499374; PubMed=11042159; DOI=10.1101/gr.145100;
2., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Okazaki Y., Muramatsu M., Hayashizaki Y.;
ation and subtraction of cap-trapper-selected cDNAs to
all-length cDNA libraries for rapid discovery of new ge
1. 10:1617-1630(2000).
Aizawa K., Akimura T., Arakawa T., Bono H., Carninci I Furuno M., Hanagaki T., Hara A., Hashizume W., K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., motani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya, Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y. Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
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3 (TrEMBLrel. 23, Last sequence update)
4 (TrEMBLrel. 27, Last annotation update)
1s adult male bone cDNA, RIKEN full-length enriched libral adult male control adult mal
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RESULT
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C TISSUE-Jaw and Limb;

X MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Hapkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length hum and mouse cDNA. sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                    Query Match
Best Local
Matches
                                                                                                                                                                                                                                                     and mouse cDNA. sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:168:
[8]

SEQUENCE FROM N.A.

TISSUE=Jaw and Limb;
Strausberg R.;
Submitted (MAR-2004) to the EMBL/Genl-!- SIMILARITY: Contains 1 SH3 domain
EMBL; AK036516; BAC29460.1; -.
EMBL; BC067208; AAH67208.1; -.
HSSP; O89100; 10EB.

GO; GO:0007242; P:intracellular signinterPro; IPR00108; Neu_cyt_fact_2.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
InterPro; IPR0011511; SH3_2.
Pfam; PF00018; SH3_1; 1.
Pfam; PF00618; SH3_1; 1.
Pfam; PF00653; SH3_2; 1.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; PS000479; DAG_PE_BIND_DOM_1; PROSITE; PS000479; DAG_PE_BIND_DOM_2; PROSITE; PS000479; DAG_PE_BIND_DOM_2; PROSITE; PS000479; SH3; 1.
 Q6TF30;
Q6TF30;
05-JUL-2004
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05-JUL-2004
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DAG_PE_BIND_DOM_2;
SH3; 1.
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i F., Takaku-Akahira S., Takeda Y., Tanaka T
    Yasunishi A., Muramatsu M., Hayashizaki Y.;
    to the EMBL/GenBank/DDBJ databases.
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RESULT
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Best Local S
Matches 7
lactofermentum' AJ12036) odhA gene encoding a novel type oxoglutarate dehydrogenase.";
Microbiology 142:3347-3354(1996).
[2]
SEQUENCE FROM N.A.
STRAIN=AJ12036;
Usuda Y., Tujimoto N., Abe C., Kimura E., Kawahara Y., Kulmatsui H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase far EMBL; D84102; BAA12222.1; -.
HSSP; P07016; 1E20.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004591; F:oxoglutarate dehydrogenase (succinyl-tra
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P96746;
01-MAY-1997 (TrE
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2-oxoglutarate c
Name=odhA;
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Neoptera; End
Ephydroidea;
NCBI_TaxID=72
                                                                                                                                                                                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
[1]
SEQUENCE FROM N.A.
STRAIN=AJ12036;
MEDLINE=97158227; PubMed=9004499;
Usuda Y., Tujimoto N., Abe C., Asakura Y., Kimura E., Kawaha:
Kurahashi O., Matsui H.;
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Name=hclA;
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                                                                                                                                                                                    cloning of the Corynebacterium glutamicum ntum' AJ12036) odhA gene encoding a novel te dehydrogenase.";
gy 142:3347-3354(1996).
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в ; Drosophilidae; Drosophila.
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(TrEMBLrel. 26, Last annotation update)
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larity 70.0%;
Conservative
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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

TS-OCT-2004 (TREMBLrel. 28, Last annotation update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

C2-OXOGLUTARATE DEHYDROCENASE).

GN Name=odhA; OrderedLocusNames=C911129, cgi280;

C3 Name=odhA; OrderedLocusNames=C91129, cgi280;

C4 Corynebacterium glutamicum (EC 1.2.4.2)

DE (2-OXOGLUTARATE DEHYDROCENASE).

C5 Bacteria, Actinobacteria, Actinobacterium (EC 1.2.4.2)

RP SEQUENCE FROM N.A.

S1 Corynebacterium glutamicum ATCC 13032.";

RR PUBMET ERM N.A.

S2 SEQUENCE FROM N.A.

S3 Bathe B., Bartels D., Bischoff N., Bott M.,

RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,

RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,

S2 SEQUENCE FROM N.A.

S3 Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Galgalat L.,

Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Galgalat L.,

Burkovski A., Dusch N., Burkols N., Fefferle W., Puehler A.,

S2 OCT-2002 Corynebacteriaceae; Corynebacteriaceae; Corynebacteriaceae;

C5 T1032 Genome sequence

C7 11032 Genome sequence
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Best Local S
Matches
"The complete Corynebacterium glutamicum ATCC 1 and its impact on the production of L-aspartate and vitamins.";

J. Biotechnol. 104:5-25(2003).
-!- SIMILARITY: Belongs to the 2-oxoacid dehydr EMBL; AP005277; BAB98522.1; -.
EMBL; BX927151; CAF19835.1; -.
HSSP; P07016; 1E2O.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0004591; F:oxoglutarate dehydrogenase (s
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00676; E1_dh; 1.
ProDom; PD001115; 20xoacid_dh; 1.
ProDom; PD001115; 20xoacid_dh; 1.
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InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR001017; Dehydrogenase_E
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003475; Transketolase_C:
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00676; E1_dh; 1.
Pfam; PF02779; Transket_pyr; 1.
ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SEQUENCE 1257 AA;
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Pred. No. 7.6e+02;
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                                                                                                                                                                                                                                                                                                                                                    activity; IEA.
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 1 C2 domain.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whice preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whice preliminary data.

EMBL; AAAB01008968; EAA13296.1; -.

R EMBL; AAAB01008968; EAA13296.1; -.

R GO; GO:0005515; F:protein binding; IEA.

InterPro; IPR000008; C2.

InterPro; IPR00098; C2.

InterPro; IPR001478; PDZ.

InterPro; IPR001478; PDZ.

R InterPro; IPR000219; RhoGEF.

Pfam; PF00168; C2; 1.

R Pfam; PF00168; C2; 1.

R PROSITE; PS50004; C2_DOMAIN_2; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50106; PDZ; 1.

INON_TER 1317 1317

SEQUENCE 1317 AA; 146724 MW; 9754561F35A3DC64 CRC64;
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                                                                                 Q811G3;
Q811G3;
Q1-JUN-2003 (1
01-JUN-2003 (1
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Son protein (1
Name=Son;
Mus musculus
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SEQUENCE FR
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Q7Q2L6;
Q1-MAR-2004
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EbiP3627 (F)
Eukaryota;
Mammalia; E
NCBI_TaxID=
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                      Metazoa; Chordata;
Eutheria; Rodentia;
=10090;
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1257 AA; 138756 MW; 96473BCB12B22ABF
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Pred. No. 7.6e+02;
3; Mismatches 2;
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Pred. No. 8e+02;
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C STRAIN=129/Sv;

X MEDLINE=20408886; PubMed=10950926; DOI=10.1006/geno.2000.6254;

X MEDLINE=20408886; PubMed=10950926; DOI=10.1006/geno.2000.6254;

X MEDLINE=20408886; PubMed=10950926; DOI=10.1006/geno.2000.6254;

X MEDLINE=20408886; PubMed=10950926; DOI=10.1006/geno.2000.6254;

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STRAIN-FVB/N; TISSUE-Kidney;

PubMed=12477932; DOI=10.1073/pnas.242603899;

K Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

K Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human in and mouse cDNA sequences.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:168:
[2]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
Director MGC Project;
Submitted (FEB-2003) to the EMBL/Gen!
EMBL; BC046419; AAH46419.1; -.
GO; GO:0005515; F:protein binding; II
NON TER 1830 1830
SEQUENCE 1830 AA; 195285 MW; B55/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
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Sciurognathi; Muridae;
..., Bono H., Kondo S.,
, suzuki H., Yamanaka I., Kiyosawa H.,
, Nogami A., Schonbach C., Gojobori T.
C., Hume D.A., Quackenbush J.,
ıda H., Batalov S., Beisel "
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cion update
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PF01

585; G-patch; 1. 0443; G_patch; 1

8353; Son. 5515; F:protein binding; IPR001159; DS_RBD. IPR000467; G_patch.

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Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gastierland T., Garibooldi M., Gissi C., Godzik A., Grough J., A. Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., A. Konagaya A., Kurochkin I.V., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., A. Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Shimada K., Vang I., Yang I., Y
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ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=Q9QX47-1. commons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration veen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regions.
SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
SIMILARITY: Contains 1 G-patch domain.
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DOMAIN: Contains 8 types of repeats which are distributed in 3
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14 X 6 AA randem repeats of [ED] -

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1-14.

3 X 11 AA tandem repats of P-S-R.

2-1.

7 X 7 AA repeats of P-S-R.

2-2.

2-3.

2-4.

2-5.

2-6.

2-7 (approximate).

2-7 (approximate).

2-8 X 19 AA repeats of P-S-R.

2-1.

3 X tandem repeats of [ST [RL] - [RK] - [RF] - S-R.

G-patch.

DRBM.

K -> F (in isoform 2).

/FTId=VSP 004416.

Missing (In isoform 2).

/FTId=VSP 004417.
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ALIGNMENTS

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RESULT 2
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CT578 hypothetical protein [imported] - Chlamydophila pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang
C;Accession: G86591
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pne
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: UNIPROT:Q9JS66; GB:BA000008; NID:g8979183;
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0809
C;Superfamily: conserved hypothetical protein TC0867
RESULT 3

F72031

Ct578 hypothetical protein - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_C;Accession: F72031

R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Clamydia pneumoniae and CA;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: F72031
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-488 < REA>
A; Cross-references: UNIPROT:Q9JS66; G:A; Experimental source: strain AR39, H:C; Genetics: A; Gene: CP1062
C; Superfamily: conserved hypothetical
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d, T.D.; Brunham, R.C.; Shen, C.; Gill, S.K.; HELUE.
Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolon
ic Acids Res. 28, 1397-1406, 2000
le: Genome sequences of Chlamydia trachomatis MoPn
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                                                                Grimwood,
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Salzberg,
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RESULT 4
D71497
hypothetical protein CT578 - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis
(serotype D,
C;Species: 13-Sep-1998 #text_change
C;Accession: D71497
R;Status: Genome sequence of an obligate intracellular pathogen o
A;Reference number: A71570; MUID:99000809; pMID:9784136
A;Accession: D71497
A;Status: preliminary
A;Accession: D71497
A;Status: preliminary
A;Cross-references: UNIPROT:084582; GB:AE001328; GB:AE001273; NI
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT578
C;Superfamily: conserved hypothetical protein TC0867
                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-491 <TET>
A;Cross-references: UNIPROT:Q9PJG2; G:A;Experimental source: strain Nigg (M:C;Genetics: A;Gene: TC0867
C;Superfamily: conserved hypothetical
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A;Molecule type: DNA
A;Residues: 1-493 <ARN>
A;Cross-references: UNIPROT:Q9Z797; GB:AE001662; GB:AE001363; NID:g4377118;
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPn0809
C;Superfamily: conserved hypothetical protein TC0867
                                                                                                                                                                                                         R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, (Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumo A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: F81655

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
F81655
                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein TC0867 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: F81655 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
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Similarity 100.0%; Pred. No. 0.00062;
.4; Conservative 0; Mismatches 0;
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  65.8%; imilarity 69.2%; Conservative
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                                                                             hypothetical protein TC0867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an obligate intracellular pathogen of humans: Chlamydia MUID:99000809; PMID:9784136
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  Score 50; DB Pred. No. 5.4; 1; Mismatches
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TPELPKPGVTPR 13

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RESULT 7
G87106
conserved hypothetical protein gc]
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_rev
C;Accession: G87106
R;Cole, S.T.; Eiglmeier, K.; Park!
R.; Davies, R.M.; Devlin, K.; Dut!
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.
A;Title: Massive gene decay in th.
A;Reference number: A86909; MUID:
A;Accession: G87106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <STO>
A;Cross-references: UNIPROT:Q9CBU
C;Genetics:
A;Gene: gcpE
C;Superfamily: gcpE protein
  RESULT 8

T14272

cortactin-binding protein 1 - rat
C; Species: Rattus norvegicus (Norway rate)
C; Date: 20-Sep-1999 #sequence_revision
C; Accession: T14272
R; Du, Y.; Weed, S.A.; Xiong, W.C.; Maranol. Cell. Biol. 18, 5838-5851, 1998
A; Title: Identification of a novel corta; Reference number: Z17952; MUID: 98414(A; Accession: T14272
A; Status: preliminary; translated from A; Molecule type: mRNA
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S55377
urPAB protein precursor - Peptostr C; Species: Peptostreptococcus magn C; Date: 15-Jul-1995 #sequence_revi C; Accession: S55377
R; de Chateau, M.; Bjoerck, L. submitted to the EMBL Data Library A; Description: Protein urPAB. A; Reference number: S55377
A; Status: preliminary
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A; Residues: 1-345 <
A; Cross-references:
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;Species: Peptostreptococcus magnus
;Date: 15-Jul-1995 #sequence_revision 01-Sep
;Accession: S55377
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revision 20-Sep-1999
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                                         1 cortactin SH3 doma 98414600; PMID:97421
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Pred. No
1; Mismat
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PMID:11234002
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glycoprotein
N;Alternate n
C;Species: hu
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RESULT VGBE18

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es: US8 n herpesvirus

human herpesvirus 3: US8

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hypothetical protein PA0371 [imported] - Pseudomonas aeruginosa (stra C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Ju
C;Accession: C83598
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, E
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, F
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83598
A;Status: preliminary
A;Residues: 1-495 <STO>
A;Residues: 1-495 <STO>
                                                                                                           RESULT 10
S36477
L2 protein - human papillomavirus type 15
C;Species: human papillomavirus type 15
C;Species: human papillomavirus type 15
C;Species: human papillomavirus type 15
C;Scession: S36477
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 19
A;Description: Primer-directed sequencing of
A;Reference number: S36469
A;Reference number: S36477
A;Molecule type: DNA
A;Residues: 1-533 <DEL>
A;Cross-references: UNIPROT: P36750; EMBL: X744
C;Superfamily: papillomavirus L2 protein
C;Keywords: late protein
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-C;Accession: A03733; A45696
R;McGeoch, D.J.; Dolan, A.; Donald, S.; Rixon, J. Mol. Biol. 181, 1-13, 1985
A;Title: Sequence determination and genetic co. A;Reference number: A00656; MUID:85160822; PMIA;Accession: A03733
A;Molecule type: DNA
A;Residues: 1-550 <MCG>
A;Cross-references: UNIPROT:P04488; GB:X02138; A;Experimental source: strain 17
R;Georgopoulou, U.; Michaelidou, A.; Roizman, J. Virol. 67, 3961-3968, 1993
A;Title: Identification of a new transcription A;Reference number: A45696; MUID:93287213; PMIA;Accession: A45696
A;Status: preliminary A;Molecule type: DNA
A;Residues: 438-550 <GEO>
A;Cross-references: GB:S62895; NID:g386127; PIA;Experimental source: R35
A;Note: sequence extracted from NCBI backbone C;Superfamily: herpesvirus glycoprotein E C;Keywords: glycoprotein E
RESULT 13
FCSOAG

IGA Fc receptor precursor - Streptococcus
N;Alternate names: beta antigen
C;Species: Streptococcus agalactiae
C;Date: 30-Jun-1992 #sequence revision 3(
C;Accession: S15330; S20240; S17038
R;Jerlstroem, P.G.; Chhatwal, G.S.; Timm:
Mol. Microbiol. 5, 843-849, 1991
A.Title: The IgA-binding beta antigen of
                                                                                                                                                                                                                                                                  T34901

probable gamma-glutamyltranspeptidase - C; Species: Streptomyces coelicolor C; Date: 05-Nov-1999 #sequence_revision C; Accession: T34901
R;Oliver, K.; Harris, D.; Parkhill, J.; submitted to the EMBL Data Library, June A; Reference number: Z21561
A; Accession: T34901
A; Status: preliminary; translated from CA; Molecule type: DNA
A; Residues: 1-603 <OLI>A; Cross-references: UNIPROT:069935; EMBL A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC3C8.26
C; Superfamily: gamma-glutamyltransferase
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C;Species: Closti
C;Date: 15-Oct-19
C;Accession: T182
R;Fujino, T.; Beg
J. Bacteriol. 179
A;Title: Organiza
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A; Accession: S20;
A; Molecule type:
A; Residues: 38-4;
R; Jerlstroem, P.(
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                       ı, P.; Aubert, J.P.
.891-1899, 1993
n of a Clostridium
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submitted to the EMBL Data Library, August 1991
A;Reference number: S17038
A;Reference number: S17038
A;Recession: S17038
A;Rocession: S17038
A;Rocession: S17038
A;Residues: 1-914, 'E', 916-1164 <JE3>
A;Residues: 1-914, 'E', 916-1164 <JE3>
A;Cross-references: EMBL:X59771; NID:g46522; PIDN:CAA42442.1; PID:C;Superfamily: IgA Fc receptor
C;Keywords: cell wall; immunoglobulin receptor; tandem repeat; traffil-37/Domain: signal sequence #status predicted <SIG>
F;38-1164/Product: IgA Fc receptor #status experimental <MAT>
F;199-438/Domain: IgA binding #status predicted <IGA1>
F;439-826/Domain: IgA binding #status predicted <IGA2>
F;827-945/Region: proline-rich repeats
F;946-1131/Domain: cell wall-spanning #status predicted <TMM>
                                                                                                                                                                                       mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 0
C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage man A;Reference number: Z22235; MUID:96355501; PMID:8702911
A;Accession: T42710
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1479 <WUK>
A;Cross-references: UNIPROT:Q64449; EMBL:U56734; NID:g1336073; PIC;Superfamily: phospholipase A2 receptor; C-type lectin homology; C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>
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A; Accession: S15330
A; Molecule type: DNA
A; Residues: 1-1164 < JER1>
A; Cross-references: UNIPROT: P27951;
A; Accession: S20240
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                                                                                                imilarity 72.
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3;
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RESULT 16
$73818
hypothetical protein H91_orf216 - Mycoplasma C; Species: Mycoplasma pneumoniae
A; Variety: ATCC 29342
C; Date: 27-Feb-1997 #sequence_revision 25-Apr C; Accession: $73818
R; Himmelreich, R.; Hilbert, H.; Plagens, H.;
Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete sequence analysis of the ge A; Reference number: $73327; MUID:97105885; PM A; Accession: $73818
A; Status: preliminary; nucleic acid sequence A; Molecule type: DNA
A; Residues: 1-216 < HIM>
A; Note: the nucleotide sequence was submitted C; Genetics:
A; Genetic code: SGC3
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A; Accession: T18262
A; Status: preliminary; t
A; Molecule type: DNA
A; Residues: 1-1664 < FUJ>
A; Cross-references: UNIF
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RESULT 20
G86550
hypothetical procession: C;Species: Chlarc;Date: 02-Mar-C;Accession: G8
R;Shirai, M.; H
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B; Laub, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hafin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A; Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647

A; Rocession: B87369

A; Residues: 1-530 <STO>
A; Cross-references: UNIPROT:Q9A9L4; GB:AE005673. ***
C; Genetics: A; Gene: CC0966
C; Superfamily: 4-co:***
                                                                                                        hypothetical protein CP0271 [imported] - Chlamydophila pneumoniae (strain AR39) C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C; Accession: F81595 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000
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F81595
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B87369

C; Species: Caulobacter crescentus
C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: B87369
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; H.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft
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Pred. No. 2.7e+02;
2; Mismatches 2;
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Venter, J.C.; Fraser, C
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l protein CPj0483 [imported] - Chlamydophila pneumoniae (strain Chlamydophila pneumoniae) Chlamydia pneumoniae Chlamydophila pneumoniae, Chlamydia pneumoniae Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

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R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brance submitted to the Protein Sequence Database, April 1995
A;Reference number: Z15789
A;Accession: T06608
A;Molecule type: DNA
A;Residues: 1-1219 <BEV>
A;Cross-references: UNIPROT:Q9SZ66; EMBL:AL049638; GSPIA;Experimental source: cultivar Columbia; BAC clone F10;Genetics:
A;Gene: ATSP:F16J13.80
A;Introns: 157;
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G72073
hypothetical protein - Chlamydophila pneu
C;Species: Chlamydophila pneumoniae, Chla
C;Date: 23-Apr-1999 #sequence_revision 23
C;Accession: G72073
R;Kalman, S.; Mitchell, W.; Marathe, R.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia
A;Reference number: A72000; MUID:99206606
A;Accession: G72073
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1043 <ARN>
A;Cross-references: UNIPROT:Q9Z868; GB:AE
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPn0483
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A; Title: Comparison of whole genome so A; Reference number: A86491; MUID:2033: A; Accession: G86550
A; Status: preliminary A; Molecule type: DNA
A; Residues: 1-1043 <STO>
A; Cross-references: UNIPROT:Q92868; G:A; Experimental source: strain J138
C; Genetics: A; Gene: CPj0483
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T06608
C;Species: Arabidopsis thaliana (mouse-ear cre C;Date: 23-Apr-1999 #sequence_revision 23-Apr-C;Accession: T06608
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E
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                                                                                                                       53.9%; ilarity 80.0%; Conservative
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of whole genome sequences of chlamydia
A86491; MUID:20330349; PMID:10871362
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MUID:99206606; PMID:10192388
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Chlamydia pneumoniae
on 23-Apr-1999 #text_o
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C48652

transfer protein spdA - Streptomyces ambofaciens plasmid pSAM2

C; Species: Streptomyces ambofaciens

C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul

C; Accession: C48652; S33428

R; Hagege, J.; Pernodet, J.L.; Sezonov, G.; Gerbaud, C.; Friedmann, A.;

J. Bacteriol. 175, 5529-5538, 1993

A; Title: Transfer functions of the conjugative integrating element pSA

A; Reference number: A48652; MUID:93374848; PMID:8366038

A; Accession: C48652

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-224 < HAG>

A; Cross-references: UNIPROT:Q07193; EMBL:Z19593; NID:g298051; PIDN:CAA

C; Genetics:

A; Genome: plasmid
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S76971
hypothetical prote
C; Species: Syneche
A; Variety: PCC 68
C; Date: 25-Apr-19
C; Accession: S769
R; Kaneko, T.; Sat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kaneko, T.; Sat
o, K.; Okumura, S
DNA Res. 3, 109-1
A;Title: Sequence
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RESULT 25

T46233
hypothetical protein T9C5.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change
C;Accession: T46233
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, Mendentted to the Protein Sequence Database, December 1999
A;Reference number: Z23026
A;Accession: T46233
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A;Accession: S76971
A;Status: nucleic acid sequence not shown; translation
A;Molecule type: DNA
A;Residues: 1-152 <KAN>
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Matches
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Superfamily:
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S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya
136, 1996
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Pred. No.
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Mewes, H.W.;

Lemcke

09-Jul-2004

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probable protein kinase - maize (fragment)
C; Species: Zea mays (maize)
C; Date: 03-Jun-1993 #sequence_revision 03-Jun-199
C; Accession: A45510
R; Biermann, B.; Johnson, E.M.; Feldman, L.J.
Plant Physiol. 94, 1609-1615, 1990
A; Title: Characterization and distribution of a ma; Reference number: A45510
A; Reference number: A45510
A; Accession: A45510
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-416 <BIE>
A; Cross-references: UNIPROT:Q02494; GB:M62985; NI
C; Superfamily: probable serine/threonine-specific
F; 26-367/Domain: protein kinase homology <KIN>
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D85070
C; Species: Arabidopsis thaliana (mouse-ea C; Date: 16-Feb-2001 #sequence_revision 16 C; Accession: D85070
R; anonymous, The European Union Arabidops Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromos A; Reference number: A85001; MUID: 20083488 A; Accession: D85070
A; Status: preliminary A; Molecule type: DNA A; Residues: 1-275 <STO> A; Cross-references: UNIPROT: Q9M0U4; GB:NC C; Genetics: A; Gene: AT4g05600 A; Map position: 4
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A;Molecule type: DNA
A;Residues: 1-261 <RIE>
A;Cross-references: UNIPH
A;Experimental source: cu
C;Genetics:
A;Map position: 3
A;Introns: 101/3; 140/2;
A;Note: T9C5.150
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Similarity 46.2%;
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RESULT 30
S43768
transcription activator VP1 - rice
C;Species: Oryza sativa (rice)
C;Date: 10-Dec-1994 #sequence_revision 26-May-1995 #te
C;Accession: S43768; S48899
R;Hattori, T.; Terada, T.; Hamasuna, S.T.
Plant Mol. Biol. 24, 805-810, 1994
A;Title: Sequence and functional analyses of the rice
A;Reference number: S43768; MUID:94250843; PMID:819330
A;Accession: S43768
A;Status: nucleic acid sequence not shown
A;Residues: 1-728 <HAT>
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 108 (transposable el C; Species: Drosophila melanogaster C; Date: 07-Mar-1988 #sequence_revision 07 C; Accession: A25684 R; Streck, R.D.; MacGaffey, J.E.; Beckendo EMBO J. 5, 3615-3623, 1986 A; Title: The structure of hobo transposab A; Reference number: A25684 A; Accession: A25684 A; Molecule type: DNA A; Residues: 1-644 <STR>A; Cross-references: UNIPROT:P12258 C; Genetics: A; Gene: FlyBase:hobo
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A;Description: T
A;Reference numb
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A;Status: preliminary; translated from GB/EMEL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-495 <GRA>
A;Cross-references: UNIPROT:O16912; EMBL:AF022972; PIDN:AAC48234.1;
A;Experimental source: strain Bristol N2; clone F10D2
C;Genetics:
A;Gene: CESP:F10D2.3
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A;Intr
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A;Cross-referen
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28717
R;Graves, T.; Wohldmann, P.; Gillam, B.
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EMBL Data Library, September 1997
he sequence of C. elegans cosmid F
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L; Mismatches 4;
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ces: UNIPROT:Q8S0A6; EMBL:D1.6640

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RESULT 31
A47521
Capsid protein - giardiavirus GLV
C;Species: giardiavirus, GLV
C;Species: giardiavirus, GLV
C;Date: 21-Jan-1994 #sequence_revision 13-Feb-1998 #text_characters: A47521
R;Wang, A.L.; Yang, H.M.; Shen, K.A.; Wang, C.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 8595-8599, 1993
A;Title: Giardiavirus double-stranded RNA genome encodes a capsidues: host Giardia lamblia
A;Reference number: A47521; MUID:93391401; PMID:8378334
A;Contents: host Giardia lamblia
A;Accession: A47521
A;Molecule type: genomic RNA
A;Residues: 1-886 <WAN>
A;Cross-references: GB:L13218; NID:g1352866; PIDN:AAB01578.1
A;Note: sequence modified after extraction from NCBI backbor C;Superfamily: giardiavirus capsid protein
C;Keywords: capsid protein
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                   RESULT 32
T19140
hypothetical protein C09G5.6 - Caen C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revis C; Date: 15-Oct-1999 #sequence_revis C; Accession: T19140
R; Palmer, S.
submitted to the EMBL Data Library, A; Reference number: Z19080
A; Accession: T19140
A; Status: preliminary; translated f A; Molecule type: DNA
A; Residues: 1-963 <WIL>
A; Cross-references: UNIPROT: Q09457; A; Experimental source: clone C09G5
C; Genetics:
A; Gene: CESP: C09G5.6
A; Map position: 2
A; Introns: 48/3; 862/3; 898/1
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Library, July 1993
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        RESULT 35
T03455
ALR protein
C; Species: H
C; Date: 24-M
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R; Wang, A.L.; Yang, H.M.; Shen, K.A.; Wang, C.C.

Proc. Natl. Acad. Sci. U.S.A. 90, 8595-8599, 1993

A; Title: Giardiavirus double-stranded RNA genome encodes a capture of the contents of t
                                                                                                                                                                                                                                                                                          large tegument protein - ateline herpe
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revisior
C;Accession: T42977
R;Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, At
A;Description: Primary structure of the A;Reference number: Z22274
A;Reference number: Z22274
A;Status: preliminary; translated from A;Status: preliminary; translated from A.Molecule type: DNA
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N; Alternate n
C; Species: gi
C; Date: 06-Fe
C; Accession:
C; Accession:
R; Wang, A.L.;
Proc. Natl. A
A; Title: Giar
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F;1-824/Domain: gag-like <GAG>
F;823-825/Region: minus-one translational frameshift
F;825-1870/Domain: pol-like <POL>

Ouerv Marti
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A;Status: preliminary; translated f1
A;Molecule type: DNA
A;Residues: 1-2471 <ALB>
A;Cross-references: UNIPROT:Q9YTK3;
A;Experimental source: strain 73
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larity 63.6%;
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Pred. No. 9.1e+02;
L; Mismatches 3;
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Mismatches 3
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the herpesvirus
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24-Mar-1999

#text_change

09-Jul-2004

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RESULT 36
T12738
ATP/GTP-binding protein 22 - Methanobacterium phage psiM2
C;Species: Methanobacterium phage psiM2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #t.
C;Accession: T12738
R;Pfister, P.; Wasserfallen, A.; Stettler, R.; Leising submitted to the EMBL Data Library, May 1998
A;Description: Archaeophage PsiM2 complete genomic DN.
A;Reference number: Z17578
A;Reference number: Z17578
A;Residues: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-144 <PFI>
A;Cross-references: UNIPROT:O80212; EMBL:AF065411; NII
A;Experimental source: host Methanobacterium thermoautorium phage psiM2 hypothetices: C;Keywords: nucleotide binding; P-loop
F;34-41/Region: nucleotide-binding motif A (P-loop)
                       T17931

IgA Fc receptor-like protein A428L - C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revisic
C;Accession: T17931
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, NA;Reference number: Z18806
A;Accession: T17931
A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-145 <GRA>
A;Cross-references: UNIPROT:Q98480; EA;Experimental source: specific host C;Genetics:
A;Note: A428L
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R; Prasad, R.; Zhadanov, A.B.; Sedkov Oncogene 15, 549-560, 1997
A; Title: Structure and expression particle: Structure and expression particle: Structure and expression particle: T03455
A; Reference number: Z14954; MUID: 973
A; Accession: T03455
A; Status: preliminary; translated find; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-4957 < PRA>
A; Cross-references: UNIPROT: O14686; C; Genetics:
A; Gene: ALR
A; Map position: 12
C; Superfamily: acute lymphoblastic log; Superfamily: acute lymphoblastic log; Reywords: alternative splicing
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PMID:9247308
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RESULT 38

B26414

95K nonspecific cross-reacting antigen - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 11-May-1989 #sequence_revision 20-Oct-1989 #text_chang
C;Accession: B26414
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identi
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: B26414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-172 <PAX>
C;Superfamily: carcinoembryonic antigen; carcinoembryonic anti
F;135-165/Domain: immunoglobulin homology <IMM>
                                                                                                                                     A; Molecule type:
A; Residues: 35-1
C; Genetics:
A; Gene: GDB: NCA
C; Superfamily: n
F; 1-138/Domain:
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A;Title: Identification of three new genes A;Reference number: A44476; MUID:93052339;
                                                                                                                                                                                                                                                                                                                                                                nonspecific cross-reacting antigen W282 precursor - human N;Alternate names: carcinoembryonic antigen homolog CGM1 (version 3) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: C40428; D44476 R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Misumi, Y.; Nakazato, H.; Matsuoka, J. Biol. Chem. 266, 11810-11817, 1991 A;Title: Molecular cloning of nonspecific cross-reacting antigens in human granulocytes. A;Reference number: A40428; MUID:91268052; PMID:2050678 A;Accession: C40428 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-177 <KUR>
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A; Accession: D44476
A; Status: preliminary; not of A; Molecule type: DNA
A; Residues: 35-141 < KHA>
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adenine phosphoribosyltransferase PA1543 [imported] - Pseudomonas aeruginosa (st C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C; Accession: F83453
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ...; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: F83453
A; Accession: F83453
A; Cross-references: UNIPROT:Q04633; GB:AE004582; GB:AE004091; NID:g9947492; PID: A; Cross-references: UNIPROT:Q04633; GB:AE004582; GB:AE004091; NID:g9947492; PID: A; Genetics: apt; PA1543
C; Superfamily: adenine phosphoribosyltransferase
Search completed: October 28, Job time: 32.6087 secs
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55018, A

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       B US-10-450-763-50962
B US-10-425-115-22781
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S US-10-425-115-22781
S US-10-425-115-22781
C US-10-425-115-22782
C US-10-425-114-6792
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US-10-450-763-50948
US-10-450-763-115-20769
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US-10-425-115-207696
Sequence 50962, A
Sequence 227818,
Sequence 227817,
Sequence 227817,
Sequence 227817,
Sequence 207691,
Sequence 37181, A
Sequence 50757, A
Sequence 37181, A
Sequence 37181, A
Sequence 50949, A
Sequence 40062, A
Sequence 40060, A
Sequence 40060, A
Sequence 50948, A
Sequence 50948, A
Sequence 70256, A
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 10, Appl
Sequence 207693, A
Sequence 207693, A
Sequence 176, App
Sequence 217317, Sequence 21848, Ap
Sequence 217317, Sequence 21848, Ap
Sequence 217317, Sequence 55940, A
Sequence 58805, A
Sequence 217317, Sequence 21848, Ap
Sequence 217317, Sequence 568032, Sequence 217317, Sequence 217317, Sequence 21848, App
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Sequence 174088, Se
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Sequence 16, Application US/10634914;
publication No. US20040029806A1;
GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES PETER
APPLICANT: MATTHEWS, RUTH CHRISTINE
TITLE OF INVENTION: MEDICAMENT
FILE REFERENCE: 050885-0281578
CURRENT APPLICATION NUMBER: US/10/634,914
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US/09/889,314
PRIOR APPLICATION NUMBER: GB 9902555.3
PRIOR APPLICATION NUMBER: GB 9902555.3
PRIOR APPLICATION NUMBER: PCT/GB00/00237
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
   Sequence 3, Application US/10634914; Publication No. US20040029806A1; GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES PETER
APPLICANT: MATTHEWS, RUTH CHRISTINE
TITLE OF INVENTION: MEDICAMENT
FILE REFERENCE: 050885-0281578
CURRENT APPLICATION NUMBER: US/10/634,914; CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US/09/889,314
PRIOR APPLICATION NUMBER: GB 9902555.3
PRIOR APPLICATION NUMBER: GB 9902555.3
PRIOR APPLICATION NUMBER: PCT/GB00/00237
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                   LENGTH: 14
; TYPE: PRT
; ORGANISM: Chlamydia
US-10-634-914-16
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US-10-634-914-
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Similarity 100.0%;
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US-09-991-073-499
US-09-990-442-499
US-09-991-163-499
US-09-993-604-499
US-09-989-721-499
US-09-989-721-499
US-09-989-735-499
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US-09-991-181-499
US-09-991-181-499
US-09-989-730-499
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RESULT 4

US-10-289-762-867
; Sequence 867, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequentiate of invention: thereof and uses thereof, in partitle OF INVENTION: and treatment of infection; FILE REFERENCE: 9710-003-999; CURRENT APPLICATION NUMBER: US/10/289,762; CURRENT FILING DATE: 2003-03-27; NUMBER OF SEQ ID NO 867
; SEQ ID NO 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-820-843A-51
; Sequence 51, Applicat;
; Publication No. US200;
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description
OTHER INFORMATION: optimised N-
OTHER INFORMATION: pneumoniae p
NAME/KEY: UNSURE
; LOCATION: (1)..(30)
; OTHER INFORMATION: S-tag and th
FEATURE:
; OTHER INFORMATION: Positions (2
US-10-634-914-3
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CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 51
LENGTH: 493
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Best Local
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: CT578 hypothetical
NAME/KEY: misc_feature
OTHER INFORMATION: gi|4377121
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ORGANISM: C
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Similarity 100.0%;
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o. US20030039963A1
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G DATE: 2001-03-30
ID NOS: 118
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APPLICANT: MATTHEWS, RUTH CHRISTINE
TITLE OF INVENTION: MEDICAMENT
FILE REFERENCE: 050885-0281578
CURRENT APPLICATION NUMBER: US/10/634,914
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US/09/889,314
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: GB 9902555.3
PRIOR APPLICATION NUMBER: PCT/GB00/00237
PRIOR APPLICATION NUMBER: PCT/GB00/00237
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                         US-10-282-122A-55018
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TITLE OF INVENTION: Identification of Electron File Reference: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,1: CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
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Publication No. US20040029806A1
GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES PETER
APPLICANT: MATTHEWS, RUTH CHRISTI
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Similarity 100.0%;
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Carr, Grant
Yamamoto, Robe
Forsyth, R.
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Malone, Cheryl
Haselbeck, Robe
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Wall, Daniel
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lio, Carlos
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
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TYPE: PRT
ORGANISM: Ch
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                                                                                                                          ORGANISM: Homo sapiens FEATURE:
NAME/KEY: DOMAIN
LOCATION: (366)..(379)
OTHER INFORMATION: LUTEOVIRUS ORF6 PROTEIN SIGNATURE domain identified by OTHER INFORMATION: eMATRIX, accession number PR00910A, p-value=1.000e-09, OTHER INFORMATION: 2.51
                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                            RENT FILING DATE: 2003-06-11

OR APPLICATION NUMBER: PCT/US01/08631

OR FILING DATE: 2001-03-30

OR APPLICATION NUMBER: 09/540,217

OR FILING DATE: 2000-03-31

OR APPLICATION NUMBER: 09/649,167

OR FILING DATE: 2000-08-23
                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R APPLICATION NUMBER: 60/253,625
R FILING DATE: 2000-11-27
R APPLICATION NUMBER: 60/257,931
R FILING DATE: 2000-12-22
R APPLICATION NUMBER: 60/267,636
R FILING DATE: 2001-02-09
R APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
APPLICATION N
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING
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                                                                    CEY: misc_feature
CON: (1)...(535)
INFORMATION: Xaa
                                                                                                                                                                                                                                         535
  8 2
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 65.8%; milarity 57.1%; Conservative
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55018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 2000-05-26
ATION NUMBER: 60/230,335
DATE: 2000-09-06
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 Score 50; DB 18;
Pred. No. 1.3e+02;
Mismatches 3
                                                                      as
                                                                      defined in Table
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••
                            Length 535;
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TPELPKPGVTPRS 14

QTPSVPKPGLEPTS

28

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PELQRPGVPP

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APPLICANT: OMUNICATION IKEDA, HARUCAPPLICANT: IKEDA, HARUCAPPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
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US-10-15
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US-10-450-763-45435
; Sequence 45435, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)...(228)
; OTHER INFORMATION: Xaa
US-10-450-763-45435
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                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                    SOFTWARE:
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Best Local S
Matches
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APPLICANT: OMURA, S
APPLICANT: IKEDA,
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Sequence 12554, Application US/10156761
Publication No. US20030119018A1
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                                                             Query Match
Best Local
                                                Matches
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TITLE OF INVENTION: NOVEL |
FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                    NUMBER OF
                                                                                                                                                                                     TYPE: PRT ORGANISM:
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ORGANISM:
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                                                                                                                                                                                                                       LENGTH:
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761-12554
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8; Conservative
                                           Similarity 66.7%;
8; Conservative
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ETPELPKPGVTP
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Pred.
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                                             ore 47; DB 18; d. No. 1.4e+02; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 1566
TYPE: POT
   В
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US-10-739-930-9579
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                                                            Query Match
Best Local S
Matches 8
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Matches 8
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Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 9579
LENGTH: 267
TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20 GENERAL INFORMATION:
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APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte
FILE REFERENCE: 021044-000330US
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                        FEATURE:
OTHER INFORMATION: human RERE
0-491-545A-63
                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo
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 758
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Similarity 57.1%;
8; Conservative
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Masuda, Esteban
Torge
   글.
                                                          61.8%; imilarity 72.7%; Conservative
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o. US20050130117A1
                                PELPKPGVTP
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X. Charlene
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Pred. No. 1.7e+02;
2; Mismatches 4;
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                                                             Score 47; DB 18;
Pred. No. 9.6e+02;
; Mismatches 2;
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                                                                                             Length 1566;
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RESULT 12 US-10-450-763-5

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RESULT 14
US-10-450-763-40067
Camuence 40067, Ap
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US-10-450-7
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches
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SEQ ID NO 5096
LENGTH: 133
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SEQ ID NO 5
LENGTH: 1
TYPE: PRI
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Publication No. US20
GENERAL INFORMATION:
                                                                  Sequence 40067, Application US/Publication No. US20050196754A1 GENERAL INFORMATION:
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Best Local
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GENERAL INFORMATION
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL I
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                           ORGANISM: F
10-450-763-9
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0-450-763-50962
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Similarity 66.7%;
B; Conservative
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Similarity 66.7%;
8; Conservative
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US20050196754A1
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      NUMBER:
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                                    NUCLEIC
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Pred. No. 1.1e
2; Mismatches
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Pred.
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No. 1
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PRIOR FILING DATE: 2003-06-11

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 40067

LENGTH: 181

TYPE: PRT

ORGANT
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369377
SEQ ID NO 227818
LENGTH: 180
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                                                                                             JS-10-425-114-67973
Sequence 67973, Application No. US200
GENERAL INFORMATION:
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ORGANISM: Zo
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Similarity 66.7%;
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                        Kovalic, Dave Screen, Steven E
         Cao, You
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o. US20040214272A1
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ou, Yihua
                                                                                                           Application US/10425114 US20040034888A1
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Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
                                               David K.
Steven E
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1; Mismatches
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ORGANISM: Zea mays; FEATURE:
COTHER INFORMATION:
US-10-425-114-67973
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US-10-425-115-
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                      NUMBER OF SEQ ID SEQ ID NO 207691 LENGTH: 259
                                       SEQ
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CURRENT FILING DATE: 2003-0
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 227817
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SEQ ID NO 67973
LENGTH: 258
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                                              APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecule,
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic A
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
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CURRENT APPLICATION
CURRENT FILING DATE:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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ORGANISM: Zea mays
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ORGANISM:
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OF SEQ ID NOS:
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Cao, Yongwei
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1; Mismatches
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Pred. No.
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US-10-425-115-227821; Sequence 227821, Application US/10425115; Publication No. US20040214272A1
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US-10-425-114-67521
; Sequence 67521, Application US/10425114
; Publication No. US20040034888A1
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TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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SEQ ID NO 227821
LENGTH: 278
TYPE: PRT
ORGANISM: Zea mays
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 67521
LENGTH: 283
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas
ADDLICANT: Kovalic, David
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Matches
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-10-425-114-67
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ORGANISM: Ze
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Score 46; DB 15;
Pred. No. 2.4e+02;
1; Mismatches 1;
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Pred. No. 2.2e+02;
; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
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US-10-450-763-50757
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                  SEQ ID NO 50
LENGTH: 29
TYPE: PRT
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EQ ID NO 37181
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0-450-763-50757
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QTPELQQPGVPP
                              ETPELPKPGVTP 12
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2; Mismatches
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Pred.
                                                             Mismatches
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5e+02
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RESULT 23 US-10-450-763-40062

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RESULT 24
US-10-450-763-50949
; Sequence 50949, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50949
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-50949
                                                                                                   RESULT 25
US-10-450-763-3
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; ORGANISM: Homo sapiens
US-10-450-763-40062
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                                                                                    Sequence 311
Publication
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                                                   APPLICANT: Hyseq, I
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Best Local
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Best Local
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                                     TITLE OF INV
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SOFTWARE: Custom
EQ ID NO 40062
LENGTH: 309
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 E OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES REFERENCE: 790CIP3/US
ENT APPLICATION NUMBER: US/10/450,763
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OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
REFERENCE: 790CIP3/US
NT APPLICATION NUMBER: US/10/450,763
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                                                                                        .84, Application US/10450763 No. US20050196754A1
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US20050196754A1
                                                      Inc
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US/10/450,763
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Pred. No. 2.6e+02;
?; Mismatches 2;
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Pred. No. 2.6e+02;
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Sequence 33421, Application US/10450763; Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763;
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
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US-10-450-763-33421
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
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Best Local S
Matches
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Best Local
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SOFTWARE: Custom
EQ ID NO 33421
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.0-450-763-33421
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R APPLICATION NUMBER: 09/54
R FILING DATE: 2000-03-31
R APPLICATION NUMBER: 09/64
R FILING DATE: 2000-08-23
ER OF SEQ ID NOS: 60736
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APPLICATION NUMBER: PCT/US01/08631
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Similarity 66.7%;
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NUMBER
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09/649,167
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2.6e+02;
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; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40060
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-40060
                       APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO!
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50948
LENGTH: 310
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; ORGANISM: Ho
US-10-450-763-48
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US-10-450-763-48965
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US-10-450-763-
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FITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO:
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763;
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
  US-10-450-7
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Matches
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Publication No
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              TYPE: PRT ORGANISM:
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8; Conservative
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Pred. No. 2.6e+02;
2; Mismatches 2
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Pred. No. 2.6e+02;
2; Mismatches 2;
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Sequence 12, Application US/09808483;
Patent No. US20020001824A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Ligand-gated anion channels of
FILE REFERENCE: Le A 34 397
CURRENT APPLICATION NUMBER: US/09/808,483
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: DE 100 136 19.2
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 18
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US-09-808-483-12
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US-10-450-763-
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
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ORGANISM: Homo
10-450-763-56923
                                                                                                   09-808-483-12
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                                                                                                                                      LENGTH:
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8; Conservative
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Similarity 66.7%;
B; Conservative
                                                Similarity 8; Conservat
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  PELPKPKLTP
                      PELPKPGVTP
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                                                                                                             melanogaster
                                                60.5%;
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                                              Score 46; DB Pred. No. 4.1e
1; Mismatches
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Pred.
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Pred.
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RESULT

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APPLICANT: Screen, Steven; APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assignment
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
Number Of SeQ ID NOS: 73128
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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NU

TITLE OF INVENTION: ARRAYS, FOR DETECTING EX

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04
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Best Local S
Matches 8
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   Matches
                 Query Match
Best Local
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APPLICANT:
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ORGANISM: Ze
FEATURE:
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                                                                                    OTHER INFORMATION: Clone ID:
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1-097-143-16572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR APPLICATION NUMBER: 60/160,191
OR FILING DATE: 1999-10-19
OR APPLICATION NUMBER: 60/161,932
OR FILING DATE: 1999-10-28
OR APPLICATION NUMBER: 60/164,769
OR APPLICATION NUMBER: 60/173,383
OR FILING DATE: 1999-11-12
OR APPLICATION NUMBER: 60/173,383
OR FILING DATE: 1999-12-28
OR APPLICATION NUMBER: 60/175,693
OR FILING DATE: 2000-01-12
OR APPLICATION NUMBER: 60/184,831
OR APPLICATION NUMBER: 60/184,831
OR APPLICATION NUMBER: 60/191,637
OR APPLICATION NUMBER: 60/191,637
OR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 1999-1
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Kovalic, David K
Screen, Steven E
Tabaska, Jack E
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Conservative
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NG DATE: 2005-04-04
ATION NUMBER: 60/157,832
DATE: 1999-10-05
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US20040034888A1
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                  60.5%;
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Score 46; DB 15; 1
Pred. No. 4.5e+02;
.; Mismatches 3;
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Pred. No. 4.1e+02;
L; Mismatches 1
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EXPRESSION OF
                                  Length 531;
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   Indels
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  Gaps
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ETPELPKPGVTP

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RESULT 35
US-10-450-763-40028
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US-09-808-483-10
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. US200200018
GENERAL INFORMATION:
APPLICANT: Bayer Akti
TITLE OF INVENTION: I
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Best Local
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Best Loc
Matches
                                                                                                  NAME/KEY: DOMAIN
LOCATION: (25)..(42)
OTHER INFORMATION: Zinc f
OTHER INFORMATION: name z
3-10-450-763-40028
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SEQ ID NO 400
LENGTH: 95
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CURRENT FILING DATE: 2001-03-
PRIOR APPLICATION NUMBER: DE 1
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: Custom
EQ ID NO 40028
                                                                                                                                                                   TYPE: PRT ORGANISM: FEATURE:
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E OF INVENTION: Ligand-gated anion
REFERENCE: Le A 34 397
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US20020001824A1
                                                 59.2%;
Similarity 66.7%;
8; Conservative
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                                                Score 45; DB Pred. No. 1.1e 2; Mismatches
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                                                                                                                 CCHC class doma E-value=5e-05,
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APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 32834

LENGTH: 156

Type. ~~~
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                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
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US-10-450-763-3
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US-10-767-701-3
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                                                            US-10-450-763-39062
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Best Local S
Matches
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Publication No
    Matches
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                 Query Matc
Best Local
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TITLE OF IN
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ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(156)
OTHER INFORMATION: unsure a
FEATURE:
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID SOFTWARE: Custom SQ ID NO 39062
                                                                                                                                                                                          ORGANISM: FEATURE:
                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(158)
OTHER INFORMATION: Xaa =
                                                                                                                                 NAME/KEY: DOMAIN
LOCATION: (89)..(106)
OTHER INFORMATION: Zinc
OTHER INFORMATION: name
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INVENTION: NOVEL NUCLEIC ACIDS AND
RENCE: 790CIP3/US
APPLICATION NUMBER: US/10/450,763
                                                                                                                                                                                                                                       158
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Similarity 61.5%;
B; Conservative
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   imilarity 66.'
; Conservative
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5. US20050196754A1
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                59.2%;
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1; Mismatches
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                 Score 45;
Pred. No.
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                                                                                                                                 CCHC class domain identified by PFam, E-value=5e-05, PFam score of 30.1
                                                                            as defined in Table
    Mismatches
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1.8e+02;
2;
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1.8e+02;
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PELPKPGVTP 12

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RESULT 40
US-10-437-963-111175
; Sequence 111175, Application US,
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
US-10-425-115-207693
; Sequence 207693, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecu
TITLE OF INVENTION: Plants and Uses THE REFERENCE: 38-21(53535)8
CURRENT APPLICATION NUMBER: US/10/767, CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 59998
LENGTH: 172
                                                                                                               8
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; OTHER INFORMATION:
US-10-425-115-207693
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; OTHER INFORMATION:
US-10-767-701-59998
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US-10-767-701-59998
                                                                                                                                                                                                                                                                                APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 207693
LENGTH: 251
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OTHER INFORMATION: Clone ID: US-10-437-963-111175
                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 111175

LENGTH: 316

TYPE: PRT

ORGANISM: Oryza sativa
FEATURE:
                                                                 Query Match
Best Local
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APPLICANT:
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Zhou, Yihua
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Barbazuk, Brad
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PT New Chlam
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                                                                                                                                                                                                                                                                                                           preventing and treating C. pneumoniae including coronary atherosclerosis.
                   16-OCT-2003
11-NOV-1996
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na; primer; assay; detection; antibody; diagnosis; infection;
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RESULT 4
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diagnosis; infection;
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RESULT 5
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                                                                                                                                         dia pneumoniae protein of 496 amino acids and treating C. pneumoniae infection and coronary atherosclerosis.
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milarity 100.0%;
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292. .302
/note= "Histidine tag"
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RESULT 6
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28-APR-1995;
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The present sequence is the dihydrofolate reductase (DHFR)/ C. pneumonipolypeptide antigen variant fusion protein. C. pneumoniae strain YK41 valued and genomic DNA extracted to prep. a lambda gtl1 DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with with myeloma P3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma The DNA obtd. was then fused with DHFR DNA and the expression vector pADA431 to give pCPN533T. The plasmid was used to transform an E. coli host, which was cultured to give an antigenic polypeptide fusion prote:
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07-NOV-1996
The present sequence is the C. pneumoniae polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPN533alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide A. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                         The present invention relates to a method for identifying candidate proteins in pathogens useful as anti-infectives. The invention discloses a computational method which involves the calculation of several sequence attributes and their subsequence analysis results in the identification of outlier proteins in different pathogens. The method is useful for the identification of outlier proteins (e.g. virulence proteins, antigens or proteins used as drug targets) in pathogenic organisms. The method of the invention provides reproducible results as it does not depend on the variable biochemical characterisation of proteins. ABO23500-ABO23617 represent outlier proteins identified from different pathogenic organisms
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RESULT

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RESULT 10
AAB08322
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Matches
                                                                                12-SEP-2003
04-DEC-2000
                                                                                                                                                                                                                                                                                                               AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)
                                                          Amino
                                                                                                                   AAB08322;
                                                                                                                                         AAB08322
                                     Chlamydia
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04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccin neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-1999.
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13-SEP-1999
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                                   pneumoniae protein;
                          therosclerosis.
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                                                                                                                                                                                                                TPELPKPGVTPRS 14
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Conservative
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                                                           sequence of a Chlamydia pneumoniae
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(first en
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98US-0107078P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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                                     infection;
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Pred. No.
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RESULT 11
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Best Local
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20-SEP-1994;
28-APR-1995;
28-APR-1995;
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Protein
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                                                             28-MAR-1996
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                                                                                                                                                                   Synthetic
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94JP-00224711.
95JP-00106006.
95JP-00106008.
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                                                                                                   Location/Qualifiers
1. .160
/label= dihydrofolat
162. .649
/label= C. pneumonia
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                                                                                                                                                                                      igen; polypeptide B; strain YK41; plasmid; r; assay; detection; antibody; diagnosis; dihydrofolate reductase; DHFR; Chlamydia
                                         95WO-JP001896
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.649
1= C. pneumoniae
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RESULT : AAY3763: ID AAY3763: 
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28-APR-1995;
28-APR-1995;
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17-DEC-1997;
04-NOV-1998;
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diagnosis of
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polypeptide
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antibody (MI
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N-PSDB; AAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is the dihydrofolate reductase (DHFR)/ C. pneumoniae peptide antigen fusion protein, polypeptide B. C. pneumoniae strain was cultured and genomic DNA extracted to prep. a lambda gtll DNA ary. The library was then screened with an anti-YK41 monoclonal body (MAb), which was prepd. by fusing spleen cells from a mouse ted with YK41 with myeloma P3/NS1/1-Ag4-1 to produce a MAb ssing hydridoma. The DNA obtd. was then fused with DHFR DNA and the sesion vector pADA431 to give pCPN533T. The plasmid was used to be peptide fusion protein, polypeptide B. Polypeptide B and primers and serived from its DNA can be used in assays for the detection of penic polypeptide antibodies and DNA, respectively, useful in the loss of C. pneumoniae infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and assay of C. pneumoniae e.g. in clinical diagnosis.
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                                                                                                                                                                                                                                                                                                                                                        trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                            ye disease; conventional trachoma; nonendemic trachoma; ma; inclusion conjunctivitis; genital disease; perihepatitis; cal uretritis; epidymitis; cervicitis; salpingitis; tis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :andard;
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95JP-00106010.
95JP-00106011.
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97FR-00016034.
98US-0107077P.
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Best Loc
Matches
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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N-PSDB;
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      invention relates to an isolated nucleic acid comprising any one 6213 antisense sequences given in the specification where expressive nucleic acid inhibits proliferation of a cell. Also included a vector comprising a promoter operably linked to the nucleic acording a polypeptide whose expression is inhibited by the antisens.
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                      ed polynucleotide and encoded polypeptides, useful in s, forensics, gene mapping, identification of mutations e for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e mapping; gene m medical imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein #15067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene mapping; gene
naging; diagnostic;
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Pred. No. 1.5e+02
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; forensic; genetic disorder.
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                                                                                                         mutations
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Claim

20;

SEQ

ID

Ö

45435;

103pp;

English

The present atrophin-1 of (II) are

: sequence represents human atrophin-1 related protein. The related gene (I), its expressed polypeptides (II) and agonists used to treat or prevent conditions requiring an increase in

are

11;

Page 25-27; 34pp; English.

atrophin-1 related gene and polypeptide useful for treating Charcote-Tooth disease and Schwartz-Jampel syndrome.

WPI; 1999-326701/27. N-PSDB; AAX56436.

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RESULT 16
AAY17406
ID AAY17406
XX
AC AAY17406;
XX
AC Human atrophin-
AC AAY17406
AAY17406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food geneplement. (II) and its binding partners are useful in medical imaging (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atrophin-1 related protein; Charcot-Marie-Tooth disease;
tz-Jampel syndrome; crystalline corneal dystrophy;
orubral pallidoluysian atrophy; ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV HUNAN MEDICAL.
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                                                                                                                                                                                                                                                                                                                                                                 Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                    Ruan
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                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1012 AA.
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Pred. No. 1.7e+02;
2; Mismatches 2;
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RESULT 17
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ID ABR59
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Best Loc
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                                                                                                                                                                                                monitoring contacting a compound.
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                                                                                                                                                                                                                                                                                Identifying a
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N-PSDB; ACC81113.
                                                                                                                                           Disclosure;
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                                                                                                                                                                                                                          y a compound that changes in cell a a T cell compris
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                                                                                                                                                                                                                       and that modulates T lymphocyte activation, useful for cell surface marker expression, comprises comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
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Mismatches
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The invention relates to a modulates T lymphocyte act: cell comprising an A-raf-1 where the A-raf-1 or TCPT

n relates to a novel method for identifying a compound lymphocyte activation. The method comprises contacting ing an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound raf-1 or TCPTP/PTPN2 polypeptide is encoded by a nucle

compound, a nucleic

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ion relates to isolated polynucleotide (I) and polypeptide (I) is useful as hybridisation probes, polymerase chain PCR) primers, oligomers, and for chromosome and gene mappi ombinant production of (II). The polynucleotides are also tics as expressed sequence tags for identifying expressed is useful in gene therapy techniques to restore normal

and polypeptide lymerase chain

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Claim

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SEQ ID NO

50962; 103pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, cell surface marker expression, cytokine production, antibody production, cell surface marker expression, cytokine production, antibody production, cell surface marker expression, and apoptosis, using either cell lines or primary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as condulation and migration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type hypersensitivity reactions, asthma, allergies, graft versus host disease, can activate and chronic inflammation. Modulators of lymphocyte activation and migration. The present sequence is used in the exemplification of the invention.
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Best Loo
Matches
                                                                                                              New isolated presponsible for biodiversity.
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23-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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Pred. No. 9.5e+02;
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ilarity 66.7%;
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            The invention relates to isolated polynucleotide (I) and polypeptide (sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorder involving aberrant protein expression or biological activity. The
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this
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sequences of the invention. Note: The sequence data for this
not appear in the printed specification, but was obtained in
format directly from WIPO at
nt/pub/published_pct_sequences
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

genes. (I) is useful in gene therapy techniques to restore normal

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supplement. (II) and its binding partners are useful in medical imaging

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involving aberrant protein expression or biological activity. The

polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

patent did not appear in the printed specification, but was obtained in

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

genes. (I) is useful in gene therapy techniques to restore normal

ctivity of (II) or to treat disease states involving (II). (II) is

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cinvolving aberrant protein expression or biological activity. The

polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

mino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

patent did not appear in the printed specification, but was obtained in

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\S67249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed polynucleotide and encoded polypeptides, useful in s, forensics, gene mapping, identification of mutations e for genetic disorders or other traits and to assess
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RESULT 31
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RESULT 32
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KW ligand-co
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pharmaceutio
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of t printed specification, but was obtained in electronic format direct from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 4.5e+02;
; Mismatches 1
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                                        New polypeptide useful in screen insecticides.
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 Thie
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                                                                                                                Franken
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                                                                                                                                                                                                                                                         ligand-controlled plant-protection a
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                                                                                                                                                                                                                                                                                                                                 AAG80005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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PSDB; AAH;
                                                                                                                                                                                                                                                                                        melanogaster
  invention
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                                                                                 2001-598685
)B; AAI68566
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AAH78309, I
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                                                                                                               (T)
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8, Conservat
                     Page
                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                 eptide subunit screening for
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                                                                                                                                                                                                                                                                                                                                                                                                       ELPKPKLTP
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                                                                                                               Friedrich
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                     31-33;
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                                                                                                                                                                                                                                                          agent;
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                                                                                                                                                                                                                                                         channel; fruitfly; insecticide; trans;
                                                 of invertebrate ligand-controlled anion potential plant-protection agents, espec
  novel
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                                                                                                             Raming
                     German
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Pred. No. 4.5e+02;
; Mismatches 1;
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                                                                                                                                                                                                                                                                                        anion
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                                                                                                                                                                                                                                                         transgenic
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                                                                                                                                                                                                                                                                    invertebrate;
 subunit
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 invertebrate
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                                                 nion channel especially
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RESULT 35
AAW56444
ID AAW56
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invention a
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Misc-differ
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                                                                                                                                                                                                                                                                      New hepatit
                                                                                                                                                                                                                                                                                                                                       WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2003
31-JUL-1998
                                              The present sequence represents a fragment of a new Hepatitis g virus protein (see also AAW56441-50 for other fragments). RNA was synthesised from the serum of nine patients judged positive for Hepatitis g virus and CDNA synthesised from this RNA. The CDNA was used as a template in several PCR reactions to isolate fragments of the new gene. The gene may be useful for diagnosing and developing treatments for Hepatitis g virus diseases. (Updated on 27-AUG-2003 to correct OS field.)
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     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                           (BMLB-)
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DB; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
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                                                                                                                                                                                                                                                                                                                                                                                                           BM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ontrolled anion channels which are useful in screening for l plant-protection agents and have insecticidal activity. The nalso describes the production of DNA constructs, vectors, host ntibodies and transgenic invertebrates which are also used in the cation of plant protection agents which alter the expression of nd controlled anion channel protein. The products of the n are also used to identify genes that encode polypeptides in insects. I polypeptides described in the specification are suitable for igh throughput assays. This sequence represents a liganded anion channel from the fruitfly Drosophila melanogaster
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                                                                                                                                                                                                                                                                                          tis G virus gene
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Conservative
                                                                                                                                                                                                                            age 101-104; 128pp; Japanese.
                                                                                                                                                                                                                                                                          virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus gene; diagnosis; treatment;
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(first en
        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-00227387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 648. .667
/note= "nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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1; Mismatches
                                                                                                                                                                                                                                                                                              useful for
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5e+02;
                                                                                                                                                                                                                                                                                             diagnosing and treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 535;
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Query Match Best Local S Matches

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60.5%; milarity 66.7%; Conservative

Score 46; DB 2; Lo Pred. No. 2.3e+03; L; Mismatches 3;

Length 2963;

0

Gaps

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ETPELPKPGVTP

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RESULT 36
ABG09669
ID ABG09
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                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cy enes. (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (involving aberrant protein expression or biological activity. The diagnostics, forensics, gene mapping, identification of mutations constituted sequences of disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in clectronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                      Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
N-PSDB; AAS73856.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
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                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                          biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                       Similarity 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ
                                                                       98
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 ETPELPKPGVTP
                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                       AA;
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2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                      59.
                                                                                                                                                                                                                                                                                                                                                                 40028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
                                 9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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maging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                103pp;
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                     Score 45; DB Pred. No. 1.4e 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                English.
                                 DB 4;
1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; forensic genetic disorder.
                                             Length 95;
                     0;
                     Gaps
                       0;
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PELQQPGVPP 82

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ABGO8703
ABGO8703
ABGO8703
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ABGO8703
ABGO8703
ABGO8703
ABGO8703
ABGO8
AC Human
KW Homo
CC Hool
ANA
AC ABGO8
AC HYSE
AC CO Gand
AC CC General
AC CC Ge
ş
                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food genement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The classostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations cannot be for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                       Query Match
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Matches
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  responsible for biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
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                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                8;
                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 39062; 103pp; English.
                                                                                                                                                                                      58 AA;
     TPELPKPGVTP 12
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                                                              59.2%;
larity 66.7%;
Conservative
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                                                         Score 45; DB 4; Le Pred. No. 2.3e+02; Mismatches 2;
                                                                                                                         Length 158;
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                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in disgnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The golypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp...wipo.int/pub/published_pct_sequences
                                                      Query Match
Best Local
Matches
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food si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73
N-PSDB; AAS71728.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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23-AUG-2000;
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                                                                                   Match
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supplement; medical imaging;
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8; Conservat
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PEKNKPGATPRT 183
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2000US-00649167.
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66.7%;
cive
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                                                   Score 44; DB Pred. No. 3.8e
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g; diagnostic;
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                                                                   DB 4;
3.8e+02;
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                                                                                Length 200;
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ELPKPGVTP

Query Match Best Local S Matches 7

Similarity

57.9%;

Conservative

2;

Score 44; DB 7; Pred. No. 4.5e+02; Pred. No. 4.5e+02;

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Indels

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Length 241;

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RESULT AD 1154 AC XX XX AC XX AC XX XX AC XX XX AC XX 
                                   This invention relates to a novel method for identifying isolated C polynucleotides that are modulated by post-transcriptional gene silencing C (PTGS). Specifically, it refers to the regulation of gene expression in C plants via PTGS and the trans-activation of homologous genes due to C increased RNA degradation. The present invention describes clusters of C polynucleotides from cereals, in particular rice, as well as homologues and the polypeptide sequences derived thereof, where gene expression is C altered in response to PTGS. As such, the elucidation of gene silencing C mechanisms can lead to more efficiently expressed transgenes, and can C also improve the understanding of plant-viral interactions and targeting C rice protein sequence that is modulated by gene silencing, given in an C exemplification of the invention. NOTE: This polypeptide sequence is a comparation of the invention. NOTE: This sequence does not appear in the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID=20030135888.
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27-MAR-2002;
04-APR-2002;
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N-PSDB; ADJ
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cereal; pla
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(WANG/)
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   Sequence
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WANG X.
CHANG H.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KATAGIRI F.
KREPS J.
MOUGHAMER T.
PROVART N.
RICKE D.
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Katagiri F,
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ant-viral interaction.
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      1 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 176; 79pp; English.
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2002US-0368327P.
2002US-0370620P.
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Kreps J, 1
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Provart N, Ricke D;
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RESULT 40
ADA54280
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Cytos
KW Cytos
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PR 21-MJ
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Yamamoto ;
Seki N, )
                                                                                                                                                                                                                                                                                                            WPI; 200
N-PSDB;
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                                                                                                                                                              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                            New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                        Claim
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(REAS-)
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24-JAN-2002; 2002US-0350435P
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                                                                                                                                           Sequence
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)B; ADA52641.
                                               281
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                                                                                          Similarity 58.3%; 7; Conservative
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ESPEHPRPGLPP
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Hio Y, Ot
Otsuka M,
           2005,
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                                                                                            Score 44; DB 6; L
Pred. No. 5.4e+02;
3; Mismatches 2;
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Otsuka K, Nagai
M, Nagahari K, M
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                                                                                                                                                                                                                                       English.
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Masuho Y;
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, Tamechika
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